

From: Bunner, Bridget  
Sent: Monday, April 04, 2005 1:15 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Hi! I'd like to request the following sequence search for case 10/056,583 (please include the pending databases):

(short peptide sequences)

1. the amino acid sequence of SEQ ID NO: 66
2. the amino acid sequence of SEQ ID NO: 96

Thanks!

Bridget Bunner

Art Unit 1647  
Rem 4C65  
(571) 272-0881  
mailbox 4C70

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: 4/4/05  
Date Completed: 4/5/05  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: 2  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: CDP  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 16:53:02 ; Search time 117.188 Seconds  
(without alignments)  
49.505 Million cell updates/sec

Title: US-10-056-583A-66  
Perfect score: 71  
Sequence: 1 EAKKYEAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	15	5	ABP52272
2	65	91.5	15	5	ABP52270
3	65	91.5	15	5	ABP52267
4	60	84.5	15	5	ABP52265
5	60	84.5	15	5	ABP52271
6	60	84.5	15	5	ABP52290
7	60	84.5	15	5	ABP52240
8	60	84.5	15	5	ABP52292
9	60	84.5	15	5	ABP52298
10	60	84.5	17	5	ABP52294
11	60	84.5	17	5	ABP52296
12	60	84.5	19	5	ABP52295
13	59	83.1	15	5	ABP52258
14	59	83.1	15	5	ABP52257
15	57	80.3	15	5	ABP52268
16	56	78.9	15	5	ABP52256
17	56	78.9	15	5	ABP52241
18	56	78.9	15	5	ABP52304
19	55	77.5	15	5	ABP52249
20	55	77.5	15	5	ABP52261
21	55	77.5	15	5	ABP52291
22	55	77.5	15	5	ABP52243
23	55	77.5	15	5	ABP52269
24	55	77.5	15	5	ABP52246
25	55	77.5	15	5	ABP52260

26	54	76.1	15	5	ABP52237	Abp52237	HLA-DR2 m
27	54	76.1	15	5	ABP52263	Abp52263	HLA-DR2 m
28	53	74.6	15	5	ABP52247	Abp52247	HLA-DR2 m
29	52	73.2	15	5	ABP52255	Abp52255	HLA-DR2 m
30	52	73.2	15	5	ABP52301	Abp52301	HLA-DR2 m
31	52	73.2	15	5	ABP52305	Abp52305	HLA-DR2 m
32	52	73.2	15	5	ABP52266	Abp52266	HLA-DR2 m
33	51	71.8	15	3	AAY58967	Aay58967	Copeptide
34	51	71.8	15	3	AAy82056	Aay82056	MHC class
35	51	71.8	15	4	AAG63191	Aag63191	Peptide w
36	51	71.8	15	5	ABP52251	Abp52251	HLA-DR2 m
37	51	71.8	15	5	ABP52297	Abp52297	HLA-DR2 m
38	51	71.8	15	5	ABP52239	Abp52239	HLA-DR2 m
39	51	71.8	15	5	ABP52274	Abp52274	HLA-DR2 m
40	51	71.8	15	7	ADJ57535	Adj57535	Cop-1 rel
41	51	71.8	15	8	ADQ59594	Adq59594	Copolymer
42	51	71.8	15	8	ADQ81221	Adq81221	Copolymer
43	51	71.8	17	5	ABP52303	Abp52303	HLA-DR2 m
44	50	70.4	15	5	ABP52226	Abp52226	HLA-DR2 m
45	50	70.4	15	5	ABP52227	Abp52227	HLA-DR2 m

ALIGNMENTS

RESULT 1	
ABP52272	ABP52272 standard; peptide; 15 AA.
XX	
AC	ABP52272;
XX	
DT	16-OCT-2002 (first entry)
XX	
DE	HLA-DR2 molecule binding peptide SEQ ID NO:66.
XX	
KW	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW	immune response; antiinflammatory; neuroprotective; proliferation;
KW	MHC class II protein inhibitor; demyelinating disease; inhibition;
KW	post-viral encephalomyelitis; post-vaccine demyelinating condition;
XX	anti-tumour necrosis factor agent.
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200259143-A2.
XX	
PD	01-AUG-2002.
XX	
PF	24-JAN-2002; 2002WO-US002071.
XX	
PR	24-JAN-2001; 2001US-0263569P.
XX	
PA	(HARD ) HARVARD COLLEGE.
XX	
PI	Strominger JL, Fridkis-Harell M;
XX	WPI; 2002-608439/65.
DR	
XX	
PT	New compositions comprising synthetic peptides in complex with a major
PT	histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT	demyelinating disease, e.g. multiple sclerosis, or post-viral
PT	encephalomyelitis.
XX	
PS	Claim 28; Page 39; 54pp; English.
XX	
CC	The present invention describes compositions (I) comprising a peptide
CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC	residues. The complex of the peptide with a major histocompatibility
CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC	immune response. (I) has antiinflammatory and neuroprotective activities,
CC	and can be used as a MHC class II protein inhibitor. The compositions
CC	comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
  
Query Match 100.0%; Score 71; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.6e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 EAKKYEAAYKAAAAA 15  
|||  
Db 1 EAKKYEAAYKAAAAA 15  
  
RESULT 2  
ABP52270  
ID ABP52270 standard; peptide; 15 AA.  
XX  
AC ABP52270;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:64.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX

SQ Sequence 15 AA;  
  
Query Match 91.5%; Score 65; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00089;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
OY 1 EAKKYEAAYKAAAAA 15  
|||  
Db 1 EAKKYEAAYKAAAAA 15  
  
RESULT 3  
ABP52267  
ID ABP52267 standard; peptide; 15 AA.  
XX  
AC ABP52267;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:61.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Example 1; Page 33; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
  
Query Match 91.5%; Score 65; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00089;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
OY 1 EAKKYEAAYKAAAAA 15



Db 1 EAKYEAYKAAAAA 15

RESULT 4

ABP52265 ID ABP52265 standard; peptide; 15 AA.

AC ABP52265;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:59.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX Homo sapiens.  
OS Synthetic.

XX WO200259143-A2.

XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Example 1; Page 33; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX Sequence 15 AA;

Query Match 84.5%; Score 60; DB 5; Length 15;  
Best Local Similarity 92.9%; Pred. No. 0.0058;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AKKYEAYKAAAAA 15  
AC 1 EAKYEAYKAAAAA 15  
DB 2 AKYEAYKAAAAA 15

RESULT 5  
ABP52271 ID ABP52271 standard; peptide; 15 AA.

XX ABP52271;

XX 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:65.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX Homo sapiens.  
OS Synthetic.

XX WO200259143-A2.

XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX Sequence 15 AA;

Query Match 84.5%; Score 60; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0058;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAKYEAYKAAAAA 15  
AC 1 EAKYEAYKAAAAA 15  
DB 1 EAKYEAYKAAAAA 15

RESULT 6  
ABP52290 ID ABP52290 standard; peptide; 15 AA.

AC ABP52290;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:84.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PS New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
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CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 84.5%; Score 60; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0058;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 EAKKYEAYKAAAAA 15  
|||  
Db 1 EAPKYEAYKAAAAA 15  
|||  
RESULT 7  
ABP52240 ID ABP52240 standard; peptide; 15 AA.  
XX  
AC ABP52240;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:34.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PS New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Example 1; Page 32; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 84.5%; Score 60; DB 5; Length 15;  
Best Local Similarity 92.9%; Pred. No. 0.0058;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 2 AKKYEAYKAAAAA 15  
|||  
Db 2 AKKYEAYKAAAAA 15  
|||  
RESULT 8  
ABP52292 ID ABP52292 standard; peptide; 15 AA.  
XX  
AC ABP52292;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:86.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX

PF 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Strominger JL, Fridkis-Hareli M;  
XX  
XX WPI; 2002-608439/65.  
XX  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a  
XX demyelinating disease, e.g. multiple sclerosis, or post-viral  
XX encephalomyelitis.  
XX  
XX  
XX Claim 28; Page 39; 54pp; English.  
XX  
XX  
XX The present invention describes compositions (I) comprising a peptide  
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
XX residues. The complex of the peptide with a major histocompatibility  
XX complex (MHC) class II HLA-DR2 protein is involved in modulating an  
XX immune response. (I) has antiinflammatory and neuroprotective activities,  
XX and can be used as a MHC class II protein inhibitor. The compositions  
XX comprising the peptides are useful for treating demyelinating diseases  
XX such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
XX demyelinating condition, and a side effect of administering an anti-  
XX tumour necrosis factor agents. The peptide further inhibits proliferation  
XX of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
XX ABP52305 represent peptides used in the exemplification of the present  
XX invention  
XX  
XX Sequence 15 AA;  
SQ  
  
Query Match 84.5%; Score 60; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0058;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EAKKYEAYKAAAAA 15  
XX |||||||  
XX 1 EAKKYEAYKAAAAA 15  
Db  
  
RESULT 9  
ABP52298  
ID ABP52298 standard; peptide; 15 AA.  
XX  
XX ABP52298;  
AC  
XX  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:92.  
DE  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
XX immune response; antiinflammatory; neuroprotective; proliferation;  
XX MHC class II protein inhibitor; demyelinating disease; inhibition;  
XX post-viral encephalomyelitis; post-vaccine demyelinating condition;  
XX anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
OS  
XX WO200259143-A2.  
PN  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX  
XX Strominger JL, Fridkis-Hareli M;  
PI

XX  
XX WPI; 2002-608439/65.  
DR  
XX  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a  
XX demyelinating disease, e.g. multiple sclerosis, or post-viral  
XX encephalomyelitis.  
XX  
XX  
XX Claim 28; Page 39; 54pp; English.  
PS  
XX  
XX  
XX The present invention describes compositions (I) comprising a peptide  
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
XX residues. The complex of the peptide with a major histocompatibility  
XX complex (MHC) class II HLA-DR2 protein is involved in modulating an  
XX immune response. (I) has antiinflammatory and neuroprotective activities,  
XX and can be used as a MHC class II protein inhibitor. The compositions  
XX comprising the peptides are useful for treating demyelinating diseases  
XX such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
XX demyelinating condition, and a side effect of administering an anti-  
XX tumour necrosis factor agents. The peptide further inhibits proliferation  
XX of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
XX ABP52305 represent peptides used in the exemplification of the present  
XX invention  
XX  
XX Sequence 15 AA;  
SQ  
  
Query Match 84.5%; Score 60; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0058;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EAKKYEAYKAAAAA 15  
XX |||||||  
XX 1 EAKKYEAYKAAAAA 15  
Db  
  
RESULT 10  
ABP52294  
ID ABP52294 standard; peptide; 17 AA.  
XX  
XX ABP52294;  
AC  
XX  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:88.  
DE  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
XX immune response; antiinflammatory; neuroprotective; proliferation;  
XX MHC class II protein inhibitor; demyelinating disease; inhibition;  
XX post-viral encephalomyelitis; post-vaccine demyelinating condition;  
XX anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
OS  
XX WO200259143-A2.  
PN  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX  
XX Strominger JL, Fridkis-Hareli M;  
PI  
XX  
XX WPI; 2002-608439/65.  
DR  
XX  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a  
XX demyelinating disease, e.g. multiple sclerosis, or post-viral  
XX encephalomyelitis.  
PT

XX Claim 28; Page 39; 54pp; English.

PS

XX The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX

XX Sequence 17 AA;

SO

Query Match 84.5%; Score 60; DB 5; Length 17;

Best Local Similarity 86.7%; Pred. No. 0.0066;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EAKKYEAYKAAAAA 15

DB 3 EAKKYEAYKAAAAA 17

RESULT 11

ABP52296

ID ABP52296 standard; peptide; 17 AA.

XX

AC ABP52296;

XX

DT 16-OCT-2002 (first entry)

XX

DE HLA-DR2 molecule binding peptide SEQ ID NO:90.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW immune response; antiinflammatory; neuroprotective; proliferation;

KW MHC class II protein inhibitor; demyelinating disease; inhibition;

KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD ) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

PT New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

PS Claim 28; Page 39; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX

XX Sequence 17 AA;

SO

Query Match 84.5%; Score 60; DB 5; Length 17;

Best Local Similarity 86.7%; Pred. No. 0.0066;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EAKKYEAYKAAAAA 15

DB 1 EAKKYEAYKAAAAA 15

RESULT 12

ABP52295

ID ABP52295 standard; peptide; 19 AA.

XX

AC ABP52295;

XX

DT 16-OCT-2002 (first entry)

XX

DE HLA-DR2 molecule binding peptide SEQ ID NO:89.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW immune response; antiinflammatory; neuroprotective; proliferation;

KW MHC class II protein inhibitor; demyelinating disease; inhibition;

KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD ) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

PT New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

PS Claim 28; Page 39; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present  
XX invention  
SQ Sequence 19 AA;  
Query Match 84.5%; Score 60; DB 5; Length 19;  
Best Local Similarity 86.7%; Pred. No. 0.0074;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EAKKYEAYKAAAAA 15  
| | | | | | | | | |  
DB 3 EAKKYEAYKAAAAA 17  
RESULT 13  
ABP52258  
ID ABP52258 standard; peptide; 15 AA.  
XX  
AC ABP52258;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:52.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Example 1; Page 33; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
Query Match 83.1%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0083;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EAKKYEAYKAAAAA 15  
| | | | | | | | | |  
DB 1 EAKKYAAYKAAAAA 15  
RESULT 14  
ABP52257  
ID ABP52257 standard; peptide; 15 AA.  
XX  
AC ABP52257;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:51.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Example 1; Page 32; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
Query Match 83.1%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0083;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EAKKYEAYKAAAAA 15  
| | | | | | | | | |  
DB 1 EAKKYAAYKAAAAA 15

## RESULT 15

ABP52268 standard; peptide; 15 AA.

AC ABP52268;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:62.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; anti-inflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
 OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M,

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.

PS Example 1; Page 33; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has anti-inflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention

SQ Sequence 15 AA;

Query Match 80.3%; Score 57; DB 5; Length 15;

Best Local Similarity 80.0%; Pred. No. 0.018;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAKKYEAYKAAAAA 15  
 ||:|||||||  
 Db 1 EAEAYKAYKAAAAA 15

Search completed: April 4, 2005, 17:26:03  
 Job time : 120.188 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:27:14 ; Search time 27.6562 Seconds  
(without alignments)  
40.488 Million cell updates/sec

Title: US-10-056-583A-66  
Perfect score: 71  
Sequence: 1 EAKKYEAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	59.2	391	4	US-09-902-540-11110 Sequence 11110, A
2	41	57.7	731	4	US-09-252-991A-18769 Sequence 18769, A
3	40.5	57.0	109	4	US-09-405-743A-7 Sequence 7, Appl1
4	40.5	57.0	109	4	US-09-816-989A-7 Sequence 7, Appl1
5	40	56.3	802	4	US-09-489-039A-11230 Sequence 11230, A
6	39	54.9	13	5	PCT-US95-04121-38 Sequence 38, Appl1
7	39	54.9	239	4	US-09-248-796A-25676 Sequence 25676, A
8	38	53.5	407	4	US-09-252-991A-29581 Sequence 29581, A
9	38	53.5	419	4	US-09-543-236-3629 Sequence 3629, Ap
10	38	53.5	576	4	US-09-543-681A-7747 Sequence 7747, Ap
11	38	53.5	730	4	US-09-902-540-16253 Sequence 16253, A
12	38	53.5	767	4	US-09-949-016-11664 Sequence 11664, A
13	38	53.5	818	4	US-09-949-016-8579 Sequence 8579, Ap
14	38	53.5	820	4	US-09-949-016-6134 Sequence 6134, Ap
15	37	52.1	13	5	PCT-US94-10257A-33 Sequence 33, Appl1
16	37	52.1	105	4	US-09-583-110-4929 Sequence 4929, Ap
17	37	52.1	111	4	US-09-471-276-1532 Sequence 1532, Ap
18	37	52.1	114	4	US-09-107-433-3514 Sequence 3514, Ap
19	37	52.1	118	4	US-09-621-976-4365 Sequence 4365, Ap
20	37	52.1	274	4	US-09-134-000C-3673 Sequence 3673, Ap
21	37	52.1	410	4	US-09-583-110-3852 Sequence 3852, Ap
22	37	52.1	413	3	US-08-669-408B-10 Sequence 10, Appl1
23	37	52.1	428	4	US-09-107-433-4072 Sequence 4072, Ap
24	37	52.1	466	4	US-09-489-039A-13950 Sequence 13950, A
25	37	52.1	552	4	US-09-634-238-338 Sequence 338, App
26	37	52.1	629	4	US-10-081-923-6 Sequence 6, Appl1
27	37	52.1	664	3	US-08-669-408B-2 Sequence 2, Appl1

28	37	52.1	669	4	US-09-878-756-4	Sequence 4, Appl1
29	37	52.1	741	4	US-09-949-016-11523	Sequence 11523, A
30	37	52.1	741	4	US-09-949-016-11524	Sequence 11524, A
31	37	52.1	3854	4	US-09-949-016-7876	Sequence 7876, Ap
32	36	50.7	13	5	PCT-US95-04121-60	Sequence 60, Appl1
33	36	50.7	54	3	US-09-117-121-30	Sequence 30, Appl1
34	36	50.7	56	4	US-09-405-743A-3	Sequence 3, Appl1
35	36	50.7	56	4	US-09-816-989A-3	Sequence 2, Appl1
36	36	50.7	109	4	US-09-645-593-2	Sequence 61141, A
37	36	50.7	171	4	US-09-270-767-61141	Sequence 27, Appl1
38	36	50.7	177	3	US-09-058-562-27	Sequence 4730, Ap
39	36	50.7	226	4	US-09-107-532A-4730	Sequence 23529, A
40	36	50.7	280	4	US-09-252-991A-23529	Sequence 4922, Ap
41	36	50.7	301	4	US-09-107-433-4922	Sequence 4018, Ap
42	36	50.7	305	4	US-09-107-433-4018	Sequence 20634, A
43	36	50.7	317	4	US-09-248-796A-20634	Sequence 2754, Ap
44	36	50.7	399	4	US-09-583-110-2754	Sequence 29504, A
45	36	50.7	422	4	US-09-252-991A-29504	

ALIGNMENTS

RESULT 1  
US-09-902-540-11110  
Sequence 11110, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 11110  
LENGTH: 391  
TYPE: PRT  
ORGANISM: Myxococcus xanthus  
US-09-902-540-11110

Query Match 59.2%; Score 42; DB 4; Length 391;  
Best Local Similarity 53.3%; Pred. No. 32;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAKKYEAYKAAAAA 15  
DB 81 KAEAYRAYKASAGSA 95

RESULT 2  
US-09-252-991A-18769  
Sequence 18769, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18769  
LENGTH: 731  
TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18769

Query Match 57.7%; Score 41; DB 4; Length 731;  
Best Local Similarity 69.2%; Pred. No. 87;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 KKYEAYKAAAAA 15  
DB 177 KIYEAYEACARA 189

## RESULT 3

US-09-405-743A-7  
; Sequence 7, Application US/09405743A  
; Patent No. 6514938  
; GENERAL INFORMATION:  
; APPLICANT: Yeda Research and Development Co., Ltd.  
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS  
; FILE REFERENCE: 60807-A  
; CURRENT APPLICATION NUMBER: US/09/405,743A  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
US-09-405-743A-7

Query Match 57.0%; Score 40.5; DB 4; Length 109;  
Best Local Similarity 66.7%; Pred. No. 15;  
Matches 12; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

OY 1 EAKKYE--AYKAAAAA 15  
DB 83 EAKKAEAAKAYKAAEAAKA 100

## RESULT 4

US-09-816-989A-7  
; Sequence 7, Application US/09816989A  
; Patent No. 6800287  
; GENERAL INFORMATION:  
; APPLICANT: Gad, Alexander  
; APPLICANT: Lis, Doris  
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKERS  
; FILE REFERENCE: 2609/60807-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/816,989A  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/101,693  
; PRIOR FILING DATE: 1998-09-25  
; PRIOR APPLICATION NUMBER: PCT/US99/22402  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentln version 3.1  
; SEQ ID NO 7  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide  
US-09-816-989A-7

Query Match 57.0%; Score 40.5; DB 4; Length 109;  
Best Local Similarity 66.7%; Pred. No. 15;  
Matches 12; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

OY 1 EAKKYE--AYKAAAAA 15

DB 83 EAKKAEAAKAYKAAEAAKA 100

## RESULT 5

US-09-489-039A-11230  
; Sequence 11230, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 11230  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-11230

Query Match 56.3%; Score 40; DB 4; Length 802;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 EAKKYEAYKAAAAA 15  
DB 375 ERKQEAEEAAAAA 389

## RESULT 6

PCT-US95-04121-38  
; Sequence 38, Application PC/TUS9504121  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Haptenated Peptides and Uses Thereof  
; NUMBER OF SEQUENCES: 62  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04121  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/222,206  
; FILING DATE: April 1, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vanstone, Darlene A.  
; REGISTRATION NUMBER: 35,279  
; REFERENCE/DOCKET NUMBER: 079.2PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6010  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
PCT-US95-04121-38

Query Match 54.9%; Score 39; DB 5; Length 13;  
Best Local Similarity 81.8%; Pred. No. 3;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



QY 5 YEAYKAAAAA 15  
|:| | | | | | | |  
Db 3 YKAKAAAAA 13

RESULT 7

US-09-248-796A-25676  
; Sequence 25676, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 25676  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-25676

Query Match 54.9%; Score 39; DB 4; Length 239;  
Best Local Similarity 71.4%; Pred. No. 58;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAKKYEAYKAAAA 14  
| | | | | | | |  
Db 131 EAKKAEAAKAAEA 144

RESULT 8

US-09-252-991A-29581  
; Sequence 29581, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29581  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29581

Query Match 53.5%; Score 38; DB 4; Length 407;  
Best Local Similarity 69.2%; Pred. No. 1.5e+02;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAKKYEAYKAAAA 13  
|:| | | | | | | |  
Db 179 EAKKAEAAKAAEA 191

RESULT 9

US-09-540-236-3629  
; Sequence 3629, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATRA  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 3629  
; LENGTH: 419  
; TYPE: PRT  
; ORGANISM: M.catarhalis  
US-09-540-236-3629

Query Match 53.5%; Score 38; DB 4; Length 419;  
Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAKKYEAYKAAAA 15  
| | | | | | | |  
Db 136 EWKREAFKKAGATA 150

RESULT 10

US-09-543-681A-7747  
; Sequence 7747, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 7747  
; LENGTH: 576  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-7747

Query Match 53.5%; Score 38; DB 4; Length 576;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAKKYEAYKAAAA 14  
|:| | | | | | | |  
Db 311 EEOFOAYKAAVAEA 324

RESULT 11

US-09-902-540-16253  
; Sequence 16253, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(115849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 16253  
; LENGTH: 730  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-16253

Query Match 53.5%; Score 38; DB 4; Length 730;

Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 AKKYEAAYKAAAA 15  
|:|:|:|:|:|  
Db 690 AQDYDALRAAGAAA 703

## RESULT 12

US-09-949-016-11664  
; Sequence 11664, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 11664  
; LENGTH: 767  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11664

Query Match 53.5%; Score 38; DB 4; Length 767;  
Best Local Similarity 64.3%; Pred. No. 2.8e+02;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 EAKKYEAAYKAAAA 14  
|||:|:|:|:|  
Db 257 EAKRREVLSAAAA 270

## RESULT 13

US-09-949-016-8579  
; Sequence 8579, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 8579  
; LENGTH: 818  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8579

Query Match 53.5%; Score 38; DB 4; Length 818;  
Best Local Similarity 64.3%; Pred. No. 3e+02;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 EAKKYEAAYKAAAA 14  
|||:|:|:|:|

Db 307 EAKKREVLSAASAA 320

## RESULT 14

US-09-949-016-6134  
; Sequence 6134, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 6134  
; LENGTH: 820  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6134

Query Match 53.5%; Score 38; DB 4; Length 820;  
Best Local Similarity 64.3%; Pred. No. 3e+02;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 EAKKYEAAYKAAAA 14  
|||:|:|:|:|  
Db 307 EAKKREVLSAASAA 320

## RESULT 15

PCT-US94-10257A-33  
; Sequence 33, Application PC/TUS9410257A  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
; APPLICANT: BRIGITTE DEVAUX  
; APPLICANT: JONATHAN B. ROTHBARD  
; APPLICANT: DAWN SMILER  
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE  
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS  
; NUMBER OF SEQUENCES: 95  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02145  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/10257A  
; FILING DATE: 1 SEPTEMBER 1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/116,824  
; FILING DATE: 03-SEP-1993  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ANNE I CRAIG  
; REGISTRATION NUMBER: 32,976  
; REFERENCE/DOCKET NUMBER: 071.1 PCT

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US94-10257A-33

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Query Match 52.1%; Score 37; DB 5; Length 13;
Best Local Similarity 81.8%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 5 YEAYKAAAAA 15
Db 3 YAAAKAAAAA 13

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Search completed: April 4, 2005, 17:47:39  
Job time : 28.6562 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: April 4, 2005, 17:21:54 ; Search time 88.5938 Seconds  
(without alignments)  
56.143 Million cell updates/sec

Title: US-10-056-583A-66  
Perfect score: 71  
Sequence: 1 EAKKYEAAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	15	US-10-056-583-66	Sequence 66, Appl
2	65	91.5	15	US-10-056-583-61	Sequence 61, Appl
3	65	91.5	15	US-10-056-583-64	Sequence 64, Appl
4	60	84.5	15	US-10-056-583-34	Sequence 34, Appl
5	60	84.5	15	US-10-056-583-59	Sequence 59, Appl
6	60	84.5	15	US-10-056-583-65	Sequence 65, Appl
7	60	84.5	15	US-10-056-583-84	Sequence 84, Appl
8	60	84.5	15	US-10-056-583-86	Sequence 86, Appl
9	60	84.5	17	US-10-056-583-88	Sequence 88, Appl
10	60	84.5	17	US-10-056-583-90	Sequence 90, Appl
11	60	84.5	19	US-10-056-583-89	Sequence 89, Appl
12	59	83.1	15	US-10-056-583-51	Sequence 51, Appl
13	59	83.1	15	US-10-056-583-52	Sequence 52, Appl

14	57	80.3	15	14	US-10-056-583-62	Sequence 62, Appl
15	56	78.9	15	14	US-10-056-583-35	Sequence 35, Appl
16	56	78.9	15	14	US-10-056-583-43	Sequence 43, Appl
17	56	78.9	15	14	US-10-056-583-50	Sequence 50, Appl
18	56	78.9	15	14	US-10-056-583-98	Sequence 98, Appl
19	55	77.5	15	14	US-10-056-583-37	Sequence 37, Appl
20	55	77.5	15	14	US-10-056-583-40	Sequence 40, Appl
21	55	77.5	15	14	US-10-056-583-54	Sequence 54, Appl
22	55	77.5	15	14	US-10-056-583-55	Sequence 55, Appl
23	55	77.5	15	14	US-10-056-583-63	Sequence 63, Appl
24	55	77.5	15	14	US-10-056-583-85	Sequence 85, Appl
25	54	76.1	15	14	US-10-056-583-31	Sequence 31, Appl
26	54	76.1	15	14	US-10-056-583-57	Sequence 57, Appl
27	53	74.6	15	14	US-10-056-583-41	Sequence 41, Appl
28	52	73.2	15	14	US-10-056-583-49	Sequence 49, Appl
29	52	73.2	15	14	US-10-056-583-60	Sequence 60, Appl
30	52	73.2	15	14	US-10-056-583-95	Sequence 95, Appl
31	52	73.2	15	14	US-10-056-583-99	Sequence 99, Appl
32	51	71.8	15	9	US-09-765-301-17	Sequence 17, Appl
33	51	71.8	15	10	US-09-765-644A-17	Sequence 17, Appl
34	51	71.8	15	14	US-10-056-583-33	Sequence 33, Appl
35	51	71.8	15	14	US-10-056-583-45	Sequence 45, Appl
36	51	71.8	15	14	US-10-056-583-68	Sequence 68, Appl
37	51	71.8	15	14	US-10-056-583-91	Sequence 91, Appl
38	51	71.8	15	14	US-10-056-583-92	Sequence 92, Appl
39	51	71.8	15	15	US-10-438-538-21	Sequence 21, Appl
40	51	71.8	17	14	US-10-056-583-97	Sequence 97, Appl
41	50	70.4	15	14	US-10-056-583-20	Sequence 20, Appl
42	50	70.4	15	14	US-10-056-583-21	Sequence 21, Appl
43	50	70.4	15	14	US-10-056-583-24	Sequence 24, Appl
44	50	70.4	15	14	US-10-056-583-42	Sequence 42, Appl
45	50	70.4	15	14	US-10-056-583-58	Sequence 58, Appl

## ALIGNMENTS

RESULT 1  
US-10-056-583-66  
; Sequence 66, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkiss-Hareli, Maisha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-66

Query Match 100.0%; Score 71; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.6e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAKKYEAAYKAAAAA 15  
DB 1 EAKKYEAAYKAAAAA 15

RESULT 2  
US-10-056-583-61

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; Sequence 61, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-61

Query Match          91.5%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00061;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 EAKKYEAYKAAAAA 15
      ||| ||| ||| ||| |||
Db      1 EAKAYEAYKAAAAA 15

RESULT 3
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64

Query Match          91.5%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00061;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 EAKKYEAYKAAAAA 15
      ||| ||| ||| ||| |||
Db      1 EAKYEAAYKAAAAA 15

RESULT 4
US-10-056-583-34
; Sequence 34, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-34

Query Match          84.5%; Score 60; DB 14; Length 15;
Best Local Similarity 92.9%; Pred. No. 0.004;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 AKKYEAYKAAAAA 15
      ||| ||| ||| ||| |||
Db      2 AKKYEAAYKAAAAA 15

RESULT 5
US-10-056-583-59
; Sequence 59, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-59

Query Match          84.5%; Score 60; DB 14; Length 15;
Best Local Similarity 92.9%; Pred. No. 0.004;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 AKKYEAYKAAAAA 15
      ||| ||| ||| ||| |||
Db      2 AKAYEAYKAAAAA 15

RESULT 6
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65

Query Match      84.5%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.004;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 EAKKYEAYKAAAAA 15
Db      1 EAKKYEAYKAAAAA 15

RESULT 7
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84

Query Match      84.5%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.004;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 EAKKYEAYKAAAAA 15
Db      1 EAKKYEAYKAAAAA 15

RESULT 8
US-10-056-583-86
; Sequence 86, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
```

```
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86

Query Match      84.5%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.004;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 EAKKYEAYKAAAAA 15
Db      1 EAKKYEAYKAAAAA 15

RESULT 9
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

Query Match      84.5%; Score 60; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0045;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 EAKKYEAYKAAAAA 15
Db      3 EAKKYEAYKAAAAA 17

RESULT 10
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized  
US-10-056-583-90

Query Match	84.5%	Score 60;	DB 14;	Length 17;
Best Local Similarity	86.7%	Pred. No. 0.0045;		
Matches 13; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

```
Qy 1 EAKKYEAYKAAAAA 15
    | |||||
Db 1 EAKAYEAYKAAAAAA 15
```

RESULT 11  
US-10-056

```

; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-89

```

Query Match	84.5%;	Score 60;	DB 14;	Length 19;
Best Local Similarity	86.7%;	Pred. No. 0.0051;		
Matches 13; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	EAKKYEAYKAAAAA	15
Db	3	EKAKEAYKAAAAAA	17

RESULT 12  
US-10-056

```

; Sequence 51, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-51

```

Query Match	83.1%;	Score 59;	DB 14;	Length 15,
Best Local Similarity	86.7%;	Pred. No.	0.0058;	

	Matches	13;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	EAKKYEAYKAAAAA	15							
Db	1	EAKKYAAYKAAAAA	15							

RESULT 13  
US-10-056-583-52

; Sequence 52, Application US/10056583  
; Publication No. US20030064915A1

; GENERAL INFORMATION:

```

; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-52

```

Query Match	83.1%	Score 59;	DB 14;	Length 15;
Best Local Similarity	86.7%;	Pred. No. 0.0058;		
Matches 13; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 EAKKYEAYKAAAAA 15  
||| ||| ||| ||| |||  
Db 1 EAKAYAAAYKAAAAA 15

RESULT 14  
US-10-056

```

; Sequence 62, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-62

```

Query Match	80.3%	Score 57;	DB 14;	Length 15;
Best Local Similarity	80.0%	Pred. No. 0.012;		
Matches 12; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0

QY 1 EAKKYEAYKAAAA 15  
||:|:|||||||  
Db 1 EAEAYKAYKAAAA 15



RESULT 15

US-10-056-583-35

; Sequence 35, Application US/10056583  
; Publication No. US20030064915A1

; GENERAL INFORMATION:

; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.

; APPLICANT: Fridkis-Hareli, Masha

; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

; TITLE OF INVENTION: CONDITIONS

; FILE REFERENCE: 24655-017

; CURRENT APPLICATION NUMBER: US/10/056,583

; CURRENT FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/263,569

; PRIOR FILING DATE: 2001-01-24

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-35

Query Match 78.9%; Score 56; DB 14; Length 15;  
Best Local Similarity 85.7%; Pred. NO. 0.018;  
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AKKYEAYKAAAAA 15  
|:|||||  
Db 2 AEKYEAYAAAAA 15

Search completed: April 4, 2005, 17:34:52  
Job time : 88.5938 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:01:24 ; Search time 24.8438 Seconds  
(without alignments)  
58.093 Million cell updates/sec

Title: US-10-056-583A-66  
Perfect score: 71  
Sequence: 1 EAKKYEAAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	59.2	188	2 I50145	homeotic protein H
2	42	59.2	289	2 A43562	homeotic protein H
3	42	59.2	950	2 T22592	hypothetical prote
4	41	57.7	254	2 H86355	probable 14-3-3 pr
5	41	57.7	728	2 H82965	DNA helicase II PA
6	40	56.3	189	2 S77930	exoskeletal protei
7	40	56.3	189	2 S77935	exoskeletal protei
8	40	56.3	1857	1 S01787	fatly-acid synthas
9	39	54.9	40	2 S58853	homeotic protein u
10	39	54.9	124	2 E84764	hypothetical prote
11	39	54.9	165	2 B87702	ribosomal protein
12	39	54.9	389	2 D26995	homeotic protein U
13	39	54.9	458	2 B87335	hypothetical prote
14	38	53.5	244	2 S40436	histone H1 - midge
15	38	53.5	261	2 T51222	hypothetical prote
16	38	53.5	265	2 S19113	cgr-4 protein - C
17	38	53.5	346	2 C82156	conserved hypothet
18	38	53.5	347	2 E83525	Tola protein PA097
19	38	53.5	428	2 E87463	hypothetical prote
20	38	53.5	513	2 G36757	probable protein A
21	38	53.5	575	2 AC0364	phosphoenolpyruvat
22	38	53.5	594	2 G70545	hypothetical glyci
23	38	53.5	735	2 T49622	hypothetical prote
24	38	53.5	760	2 I58159	protein kinase C-r
25	38	53.5	760	2 S55473	chloride channel 3
26	38	53.5	820	2 I37240	chloride channel p
27	38	53.5	1239	1 Q0BE10	BOLFI protein - hu
28	37	52.1	170	2 G81426	H+-transporting tw
29	37	52.1	201	2 A81120	conserved hypothet

30	37	52.1	292	2 T40637	40s ribosomal prot
31	37	52.1	339	2 S39979	chitinase (EC 3.2.
32	37	52.1	340	2 S40414	chitinase (EC 3.2.
33	37	52.1	361	2 T12470	hypothetical prote
34	37	52.1	373	2 A69773	hypothetical prote
35	37	52.1	384	2 D81007	GTP-binding protei
36	37	52.1	413	2 S55890	plasma protein rec
37	37	52.1	420	2 B75333	twitching mobility
38	37	52.1	490	2 I41024	colicin 10 - Esche
39	37	52.1	525	2 A45053	proteinase RPI - R
40	37	52.1	527	2 E69351	phosphoglycerate d
41	37	52.1	537	2 AF2785	lipoprotein (impor
42	37	52.1	562	2 H97564	43k antigen (AF157
43	37	52.1	573	2 H82257	phosphoenolpyruvat
44	37	52.1	577	2 F98004	phosphoenolpyruvat
45	37	52.1	577	2 D95136	phosphoenolpyruvat

## ALIGNMENTS

RESULT 1  
I50145  
homeotic protein Hox M - chicken  
N/Alternate names: CHOX M  
C/Species: Gallus gallus (chicken)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004  
C/Accession: I50145; S14512  
R/Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.  
Leukemia 5, 357-360, 1991  
A/Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic vi  
A/Reference number: I50145; MUID:91238215; PMID:1674560  
A/Accession: I50145  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-188 <CRO>  
A/Cross-references: UNIPROT:P23459; EMBL:X57158; NID:962700; PIDN:CAA40445.1; PID:96270  
C/Genetics:  
A/Gene: CHOX M  
C/Superfamily: homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/96-152/Domain: homeobox homology <Hox>

Query Match 59.2%; Score 42; DB 2; Length 188;  
Best Local Similarity 81.8%; Pred. No. 10;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 YEAYKAAAAA 15  
Db 10 YSKYKAAAAA 20

RESULT 2  
A43562  
homeotic protein Hox D8 - mouse  
N/Alternate names: homeotic protein Hox 4.3  
C/Species: Mus musculus (house mouse)  
C/Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 09-Jul-2004  
C/Accession: A43562  
R/Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zapavigna, V.; Falkenstein, H.; Dubo  
Development 110, 733-745, 1990  
A/Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeot  
A/Reference number: A43562; MUID:91209232; PMID:1982431  
A/Accession: A43562  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-289 <IZP>  
A/Cross-references: UNIPROT:P23463  
C/Superfamily: homeotic protein Hox A7; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/196-252/Domain: homeobox homology <Hox>

Query Match 59.2%; Score 42; DB 2; Length 289;

Best Local Similarity 81.8%; Pred. No. 16;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAAA 15  
| | | | | | | | | |  
DB 10 YSKYKAAAAA 20

## RESULT 3

T22592

hypothetical protein F53H10.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T22592

R/Wilkinson, J.

submitted to the EMBL Data Library, July 1996

A/Reference number: Z19586

A/Accession: T22592

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-950 &lt;WIL&gt;

A/Cross-references: UNIPROT:Q20733; EMBL:Z77664; PIDN:CAB01216.1; GSPDB:GN00023; CESP:FS

A/Experimental source: clone F53H10

C/Genetics:

A/Gene: CESP:F53H10.2

A/Map position: 5

A/Introns: 89/3; 124/3; 151/3; 201/3; 236/3; 267/2; 293/3; 340/2; 393/3; 501/2; 550/1; 6

## Query Match

Best Local Similarity 59.2%; Score 42; DB 2; Length 950;  
Best Local Similarity 66.7%; Pred. No. 48;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 EAKKYEAYKAAAAA 15  
| | | | | | | | | |  
DB 817 EAKAHDAQVAAAAA 831

## RESULT 4

H86355

probable 14-3-3 protein T16E15.8 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: H86355

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

aneen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: H86355

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-254 &lt;STO&gt;

A/Cross-references: UNIPROT:P48347; GB:AE005172; NID:g9392684; PIDN:AAF87261.1; GSPDB:GN

C/Genetics:

A/Map position: 1

C/Superfamily: 14-3-3 protein

## Query Match

Best Local Similarity 57.7%; Score 41; DB 2; Length 254;  
Best Local Similarity 90.0%; Pred. No. 20;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 EAYKAAAAA 15  
| | | | | | | | | |  
DB 151 EAYKAAVAAA 160

## RESULT 5

H82965  
DNA helicase II PA5443 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C/Accession: H82965

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lozy, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: H82965

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-728 &lt;STO&gt;

A/Cross-references: UNIPROT:Q9L7T3; GB:AE004957; GB:AE004091; NID:g9951770; PIDN:AAG0882

A/Experimental source: strain PA01

C/Genetics:

A/Gene: uvrd; PA5443

C/Superfamily: helicase II

## Query Match

Best Local Similarity 57.7%; Score 41; DB 2; Length 728;  
Best Local Similarity 69.2%; Pred. No. 55;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 KKYEAYKAAAAA 15  
| | | | | | | | | |  
DB 174 KIYEAYEAAACARA 186

## RESULT 6

S77930  
exoskeletal protein HACP202A - American lobster (fragment)

C/Species: Homarus americanus (American lobster)

C/Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004

C/Accession: S77930

R/Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.

submitted to the Protein Sequence Database, June 1997

A/Description: Characterization of exoskeletal proteins from the American lobster, Homar

A/Reference number: S77925

A/Accession: S77930

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-189 &lt;NOU&gt;

A/Cross-references: UNIPROT:Q7M496

## Query Match

Best Local Similarity 56.3%; Score 40; DB 2; Length 189;  
Best Local Similarity 53.3%; Pred. No. 22;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 EAKKYEAYKAAAAA 15  
| | | | | | | | | |  
DB 12 KARFPQAFKAAEAAA 26

## RESULT 7

S77935

exoskeletal protein HACP202B - American lobster (fragment)

C/Species: Homarus americanus (American lobster)

C/Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004

C/Accession: S77935

R/Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.

submitted to the Protein Sequence Database, June 1997

A/Description: Characterization of exoskeletal proteins from the American lobster, Homa

A/Reference number: S77925

A/Accession: S77935

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-189 &lt;NOU&gt;

A/Cross-references: UNIPROT:Q7M495

## Query Match

Best Local Similarity 56.3%; Score 40; DB 2; Length 189;  
Best Local Similarity 53.3%; Pred. No. 22;





Query Match 53.5%; Score 38; DB 2; Length 261;  
Best Local Similarity 71.4%; Pred. NO. 65;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AKKYEAAYKAAAAA 15  
| | | | | | | | | |  
Db 116 APKQEQSKAAAAA 129

Search completed: April 4, 2005, 17:27:05  
Job time : 29.8438 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:02:08 ; Search time 111.094 Seconds

(without alignments)  
69.141 Million cell updates/sec

Title: US-10-056-583A-66  
Perfect score: 71  
Sequence: 1 EAKKYEAYKAAAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	47	66.2	840	2 Q6MBW7	Q6mbw7 parachlamyd
2	46	64.8	1038	2 Q8MQW9	Q8mqw9 drosophila
3	46	64.8	2347	2 Q8IMN9	Q8imn9 drosophila
4	46	64.8	2451	2 Q9VG05	Q9vg05 drosophila
5	45	63.4	847	2 Q6M9S8	Q6m9s8 parachlamyd
6	45	63.4	867	2 Q6MBH0	Q6mbh0 parachlamyd
7	44	62.0	380	2 Q8W0D1	Q8w0d1 oryza sativ
8	44	62.0	390	2 Q615H3	Q615h3 oryza sativ
9	44	62.0	853	2 Q7S637	Q7s637 neurospora
10	42	59.2	188	1 HXDB_CHICK	P23459 gallus gall
11	42	59.2	235	2 Q8S703	P23463 oryza sativ
12	42	59.2	289	1 HXDB_MOUSE	P23463 oryza sativ
13	42	59.2	289	2 Q81XZ1	Q81xz1 homo sapien
14	42	59.2	290	1 HXDB_HUMAN	Q6ay89 rattus norv
15	42	59.2	364	2 Q6AY89	Q6ay89 rattus norv
16	42	59.2	391	2 Q8KRC9	Q8krc9 myxococcus
17	42	59.2	900	2 Q20733	Q20733 caenorhabdi
18	41	57.7	131	2 Q89D24	Q89d24 bradyrhizob
19	41	57.7	183	2 Q8R294	Q8r294 oryza sativ
20	41	57.7	254	1 143A_ARATH	P48347 arabidopsis
21	41	57.7	319	2 Q8T762	Q8t762 branchiosto
22	41	57.7	361	2 Q8C7Q4	Q8c7q4 mus musculu
23	41	57.7	728	2 Q917T3	Q917t3 pseudomonas
24	41	57.7	847	2 Q7SC23	Q7sc23 neurospora
25	40	56.3	189	2 Q7M495	Q7m495 homarus ame
26	40	56.3	189	2 Q7M496	Q7m496 homarus ame
27	40	56.3	232	2 Q6MCQ7	Q6mcq7 ixodes scap
28	40	56.3	237	2 Q6C1J7	Q6c1j7 yarrowia li
29	40	56.3	466	2 Q64Z47	Q64z47 bacteroides
30	40	56.3	512	2 Q7XVB8	Q7xvb8 oryza sativ
31	40	56.3	575	2 Q7WWX1	Q7wwx1 alcaligenes

32	40	56.3	603	2 Q64JV8	Q64jv8 plasmodium
33	40	56.3	608	2 Q64JV9	Q64jv9 plasmodium
34	40	56.3	608	2 Q64TW1	Q64jw1 plasmodium
35	40	56.3	614	2 Q64JV2	Q64jv2 plasmodium
36	40	56.3	727	2 Q64UT8	Q64jv8 plasmodium
37	40	56.3	727	2 Q64UV3	Q64jv3 plasmodium
38	40	56.3	727	2 Q64UV7	Q64jv7 plasmodium
39	40	56.3	746	2 Q9W4M9	Q9w4m9 drosophila
40	40	56.3	747	2 Q7PIN7	Q7pin7 anopheles g
41	40	56.3	751	2 Q97427	Q97427 drosophila
42	40	56.3	765	2 Q9XB76	Q9xbt6 klebsiella
43	40	56.3	785	2 Q869D8	Q869d8 ascidia syd
44	40	56.3	810	2 Q64JV4	Q64jv4 plasmodium
45	40	56.3	822	2 Q81QN2	Q81qn2 drosophila

ALIGNMENTS

RESULT 1					
ID	Q6MBW7	PRELIMINARY;	PRT;	840 AA.	
AC	Q6MBW7;				
DT	05-JUL-2004 (TREMBlrel. 27, Created)				
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)				
DE	Hypothetical protein.				
GN	OrderedLocustNames=pc1208;				
OS	Parachlamydia sp. (subsp. Acanthamoeba sp.).				
OC	Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.				
OX	NCBI_TaxID=264201;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,				
RA	Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,				
RA	Rattei T., Mewes H.-W., Wagner M.;				
RT	"Genome sequence of an amoeba symbiont and its use for reconstructing				
RT	the evolutionary history of chlamydiae."				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BX908798; CAP23932.1; "				
KW	Complete proteome; Hypothetical protein.				
SQ	SEQUENCE 840 AA; 96146 MW; 1F1542949F953C4D CRC64;				
Query Match					
Best Local Similarity 66.2%; Score 47; DB 2; Length 840;					
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
OY	1 EAKKYEAYKAA 11				
DB	712 EAKKYEAYKAA 722				
RESULT 2					
ID	Q8MQW9	PRELIMINARY;	PRT;	1038 AA.	
AC	Q8MQW9;				
DT	01-OCT-2002 (TREMBlrel. 22, Created)				
DT	01-OCT-2002 (TREMBlrel. 22, Last sequence update)				
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)				
DE	SD05989p (Fragment).				
GN	ORFNames=CG7518;				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Stapleton M., Brokslein P., Hong L., Agbayani A., Carlson J.,				
RA	Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,				
RA	George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,				
RA	Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,				
RA	Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,				

RA Celniker S.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY122252; AAM52764.1; -.  
DR FlyBase; FBgn0038108; CG7518.  
FT NON TER 1 1  
SQ SEQUENCE 1038 AA; 109059 MW; 80C935A2C6D8A276 CRC64;  
  
Query Match 64.8%; Score 46; DB 2; Length 1038;  
Best Local Similarity 73.3%; Pred. No. 86;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EAKKYEAYKAAAAA 15  
Db 101 KAKKKEAKRAAAAAA 115  
  
RESULT 3  
Q8INH9 PRELIMINARY; PRT; 2347 AA.  
AC Q8INH9;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE CG7518-PA.  
GN ORFNames=CG7518;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,  
RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Mista S., Crosby M.A., Nungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003698; AAN14338.1; -.  
DR IntAct; Q8INH9; -.  
DR FlyBase; FBgn0038108; CG7518.  
DR InterPro; IPR001005; Myb\_DNA\_binding.  
DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
SQ SEQUENCE 2347 AA; 257013 MW; 23BF5FC5FFCAEA64 CRC64;  
  
Query Match 64.8%; Score 46; DB 2; Length 2347;  
Best Local Similarity 73.3%; Pred. No. 1.8e+02;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EAKKYEAYKAAAAA 15  
Db 1363 KAKKKEAKRAAAAAA 1377  
  
RESULT 4  
Q9VG05 PRELIMINARY; PRT; 2451 AA.  
AC Q9VG05;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE CG7518-PA.  
GN ORFNames=CG7518;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
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RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S.E., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe W., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabot G.L.,  
RA Abrell J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Paclebj M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*";  
RL Science 287:2185-2195(2000).  
RN [2]  
  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Paclebj J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:::  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whittifed E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review."  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]

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RP      SEQUENCE FROM N.A.
RG      FlyBase;
RL      Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN      [6]
RP      SEQUENCE FROM N.A.
RG      FlyBase;
RL      Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AE003698; AAF54888.2; -.
DR      FlyBase; FBgn0038108; CG7518.
DR      InterPro; IPR001005; Myb_DNA_binding.
SQ      PROSITE; PS00037; MYB_1; UNKNOWN_1.
SQ      SEQUENCE      2451 AA; 266959 MW; 088A2293F27481E2 CRC64;

Query Match
Best Local Similarity      64.8%; Score 46; DB 2; Length 2451;
Matches      11; Conservative      2; Mismatches      2; Indels      0; Gaps      0;

QY      1      EAKKYEAYKRAAAAAA      15
          :|||||:|||||
Db      1363      KAKKKEAKRAAAAAA      1377

RESULT 5
Q6M9S8      PRELIMINARY;      PRT;      847 AA.
AC      Q6M9S8;
DT      05-JUL-2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, last sequence update)
DT      05-JUL-2004 (TREMBlrel. 27, last annotation update)
DE      Hypothetical protein.
GN      OrderedLocustNames=pc1947;
OS      Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC      Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX      NCBI_TaxId=264201;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA      Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA      Rattei T., Mewes H.-W., Wagner M.;
RT      "Genome sequence of an amoeba symbiont and its use for reconstructing
RL      the evolutionary history of chlamydiae.";
RL      Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BX908798; CAF24671.1; -.
KW      Complete proteome; Hypothetical protein.
SQ      SEQUENCE      847 AA; 97399 MW; 75C178870938FF21 CRC64;

Query Match
Best Local Similarity      63.4%; Score 45; DB 2; Length 847;
Matches      8; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      1      EAKKYEAYKA      10
          |||:|||||
Db      723      EAKRYEAYKS      732

RESULT 6
Q6MBH0      PRELIMINARY;      PRT;      867 AA.
AC      Q6MBH0;
DT      05-JUL-2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, last sequence update)
DT      05-JUL-2004 (TREMBlrel. 27, last annotation update)
DE      Hypothetical protein.
GN      OrderedLocustNames=pc1355;
OS      Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC      Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX      NCBI_TaxId=264201;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA      Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA      Rattei T., Mewes H.-W., Wagner M.;
RT      "Genome sequence of an amoeba symbiont and its use for reconstructing

```

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RT the evolutionary history of chlamydiae."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF24079.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 867 AA; 99667 MW; 84B67A53CD342E32 CRC64;

Query Match
Best Local Similarity 63.4%; Score 45; DB 2; Length 867;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKYEAYKA 10
Db 739 EAKRYEAYKS 748

RESULT 7
Q8W0D1 PRELIMINARY; PRT; 380 AA.
AC Q8W0D1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative nuclear RNA binding protein A.
GN Name=P0690B02.20;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1."
RL Nature 420:312-316(2002).
DR EMBL; AP003292; BAB8432.1; -
DR Gramene; Q8W0D1; -
DR Pfam; PF04774; HABP4_PAI-RBP1; 1.
SQ SEQUENCE 380 AA; 40426 MW; 2B7C9916D9162194 CRC64;

Query Match
Best Local Similarity 62.0%; Score 44; DB 2; Length 380;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AKKYEAYKAAAAA 15
Db 29 AOKAEAKKAAAAA 42

RESULT 8
Q615H3 PRELIMINARY; PRT; 390 AA.
AC Q615H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein OSJNBa0053E05.13.
GN Name=OSJNBa0053E05.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Liew H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC121365; AAT47083.1; -
DR InterPro; IPR006861; HABP4_PAI-RBP1.
DR Pfam; PF04774; HABP4_PAI-RBP1; 1.
KW Hypothetical protein.
SQ SEQUENCE 390 AA; 41958 MW; 445445FF0E18B299 CRC64;

Query Match
Best Local Similarity 62.0%; Score 44; DB 2; Length 390;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AKKYEAYKAAAAA 15
Db 29 AOKAEAKKAAAAA 42

RESULT 9
Q7S637 PRELIMINARY; PRT; 853 AA.
AC Q7S637;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein B15B10.130.
GN Name=NCU04772.1; Synonyms=B15B10.130;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehan B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd C., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seltzer S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100031; EAA30985.1; -
DR EMBL; BX897677; CAE85580.1; -
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KW Hypothetical protein.  
SQ SEQUENCE 853 AA; 94019 MW; 505BF08C7CB6827D CRC64;

Query Match 62.0%; Score 44; DB 2; Length 853;  
Best Local Similarity 73.3%; Pred. No. 1.5e+02;  
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 EAKKYEAYKAAAAA 15  
Db 671 EAKKEAEKAAAAA 685

## RESULT 10

ID HXD8\_CHICK STANDARD; PRT; 188 AA.  
AC P23459;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Homeobox protein Hox-D8 (Chox-M).  
GN Name=HOXD8; Synonyms=CHOX-M;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91238215; PubMed=1674560;  
RA Crompton M.R., McGregor A.D., Goodwin G.H.;  
RT "cDNA cloning of a homeobox-containing gene expressed in avian  
RT myeloblastic virus-transformed chicken monoblastic leukaemia cells.";  
RL Leukemia 5:357-360(1991).  
CC -!- FUNCTION: Sequence-specific transcription factor which is part of  
CC a developmental regulatory system that provides cells with  
CC specific positional identities on the anterior-posterior axis.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: Belongs to the Antp homeobox family.  
CC -!- SIMILARITY: Contains 1 homeobox domain.  
CC -----  
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CC -----  
DR EMBL; X57158; CAA40445.1; -.  
DR PIR; I50145; I50145.  
DR HSSP; P02833; 9ANT.  
DR TRANSFAC; T01754; -.  
DR InterPro; IPR001827; Antennapedia.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain like.  
DR InterPro; IPR000447; HTH\_lambdarepressr.  
DR Pfam; PF00046; Homeobox; 1.  
DR PRINTS; PR00025; ANTENNAPEDIA.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRINTS; PR00031; HTHREPRESSR.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;  
KW Transcription regulation.  
FT DOMAIN 15 25 Poly-Ala.  
FT SITE 83 88 Antp-type hexapeptide.  
FT DNA\_BIND 95 154 Homeobox.  
SQ SEQUENCE 188 AA; 21729 MW; D4560B8807FE29FE CRC64;

Query Match 59.2%; Score 42; DB 1; Length 188;

Best Local Similarity 81.8%; Pred. No. 79;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAAAA 15  
Db 10 YSKYKAAAAAA 20

## RESULT 11

ID Q8S703 PRELIMINARY; PRT; 235 AA.  
AC Q8S703;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Putative glutathione S-transferase.  
GN Name=OSJNBa0034L04.24; ORFNames=OSJNBd0038A07.37;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22195796; PubMed=12207219; DOI=10.1007/s00438-002-0706-1;  
RA Yuan Q., Hill J., Hsiao J., Moffat K., Ouyang S., Cheng Z., Jiang J.,  
RA Buell C.R.;  
RT "Genome sequencing of a 239-kb region of rice chromosome 10L reveals a  
RT high frequency of gene duplication and a large chloroplast DNA  
RT insertion.";  
RL Mol. Genet. Genomics 267:713-720(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Buell R.;  
RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,  
RA Overton II L.L., Bera J.J., Taitlin T., Krol M.I., Jarrahi B.B.,  
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,  
RA Uterback T.T., Feldblum T.V., Yang Q.Q., Haas B.J., Suh B.B.,  
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;  
RN Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA The Rice Chromosome 10 Sequencing Consortium;  
RT "In-depth view of structure, activity, and evolution of rice  
RT chromosome 10.";  
RL Science 300:1566-1569(2003).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;  
RN Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the GST superfamily.  
DR EMBL; AC091680; AAM12328.1; -.  
DR EMBL; AC113948; AAM94508.1; -.  
DR EMBL; AE017114; AAP54743.1; -.  
DR HSSP; O04941; IGWC.  
DR Gramene; Q8S703; -.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR InterPro; IPR004046; GST\_Cterm.  
DR InterPro; IPR010987; GST\_C like.  
DR InterPro; IPR004045; GST\_Nterm.  
DR Pfam; PF00043; GST\_C; 1.  
DR Pfam; PF02798; GST\_N; 1.  
KW Transferrase.  
SQ SEQUENCE 235 AA; 25461 MW; 6FB0C8F156C8B45B CRC64;

Query Match 59.2%; Score 42; DB 2; Length 235;  
Best Local Similarity 71.4%; Pred. No. 97;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 AKKYEAYKAAAAA 15



Db 220 AKKROAERAAAAA 233

## RESULT 12

HXD8\_MOUSE STANDARD; PRT; 289 AA.  
 ID HXD8\_MOUSE  
 AC P23463;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Homeobox protein Hox-D8 (Hox-4.3) (Hox-5.4).  
 GN Name=Hoxd8; Synonyms=Hox-4.3, Hoxd-8;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91209232; PubMed=1982431;  
 RA Izpisua-Belmonte J.-C., Dolle P., Renucci A., Zappavigna V.,  
 RA Falkenstein H., Duboule D.;  
 RT "Primary structure and embryonic expression pattern of the mouse Hox-  
 RT 4.3 homeobox gene.";  
 RL Development 110:733-745 (1990).  
 RN [2]  
 RP SEQUENCE OF 191-289 FROM N.A.  
 RX MEDLINE=91274361; PubMed=1675873; DOI=10.1016/0167-4781(91)90020-M;  
 RA Sadoul R., Featherstone M.;  
 RT "Sequence analysis of the homeobox-containing exon of the murine Hox-  
 RT 4.3 homeogene.";  
 RL Biochim. Biophys. Acta 1089:259-261 (1991).  
 RN [3]  
 RP SEQUENCE OF 195-254 FROM N.A.  
 RX MEDLINE=92073356; PubMed=1683707;  
 RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,  
 RA Copeland N.G., Potter S.S.;  
 RT "Identification of 10 murine homeobox genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710 (1991).  
 RN [4]  
 RP SEQUENCE OF 192-260 FROM N.A.  
 RX MEDLINE=92212934; PubMed=1348361;  
 RA Nazarali A., Kim Y., Nirenberg M.;  
 RT "Hox-1.1 and Hox-4.9 homeobox genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2883-2887 (1992).  
 CC -1- FUNCTION: Sequence-specific transcription factor which is part of  
 CC a developmental regulatory system that provides cells with  
 CC specific positional identities on the anterior-posterior axis.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: Belongs to the Antp homeobox family.  
 CC -1- SIMILARITY: Contains 1 homeobox domain.  
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 CC -----  
 DR EMBL; X56561; CAA39911.1; -;  
 DR EMBL; M87803; AAA37852.1; -;  
 DR PIR; A43562; A43562.  
 DR PIR; S16177; A41605.  
 DR HSSP; P02833; 9ANT.  
 DR TRANSFAC; T01426; -;  
 DR MGD; MGI:96209; Hoxd8.  
 DR InterPro; IPR001827; Antennapedia.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR009057; Homeoboxdomain\_like.  
 DR Pfam; PF00046; Homeobox; 1.  
 DR PRINTS; PR00025; ANTENNAPEIDIA.  
 DR PRINTS; PR00024; HOMEBOX.

ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00032; ANTENNAPEIDIA; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;  
 KW Transcription regulation.

FT	DOMAIN	15	28	Poly-Ala.
FT	DOMAIN	62	89	Gly/Pro-rich.
FT	DOMAIN	108	117	Poly-Pro.
FT	SITE	183	188	Antp-type hexapeptide.
FT	DNA BIND	195	254	Homeobox.
FT	CONFLICT	207	208	TL -> RV (in Ref. 1).
FT	CONFLICT	231	231	T -> S (in Ref. 1).
FT	CONFLICT	265	266	EA -> DG (in Ref. 1).
FT	CONFLICT	275	275	A -> V (in Ref. 2).
SC	SEQUENCE	289 AA;	31410 MW;	5783099F9B2BDFE CRC64;

Query Match 59.2%; Score 42; DB 1; Length 289;  
 Best Local Similarity 81.8%; Pred. No. 1.2e+02;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 YEAYKAAAAA 15  
 Db 10 YSKYKAAAAA 20

## RESULT 13

Q8IXZ1 PRELIMINARY; PRT; 289 AA.

ID Q8IXZ1  
 AC Q8IXZ1;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Homeo box D8.  
 GN Name=HOXD8;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Gimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; BC038709; AAH38709.1; -;  
 DR HSSP; P02833; 9ANT.  
 DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001827; Antennapedia.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain\_like.  
DR Pfam; PF00046; Homeobox\_1.  
DR PRINTS; PR00025; ANTENNAPEIDIA.  
DR PRINTS; PR00024; HOMEBOX.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00032; ANTENNAPEIDIA; UNKNOWN\_1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
DR DNA-binding; Homeobox; Nuclear protein.  
SQ SEQUENCE 289 AA; 31839 MW; 4C2621085174B447 CRC64;

Query Match 59.2%; Score 42; DB 2; Length 289;  
Best Local Similarity 81.8%; Pred. No. 1.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAAA 15  
| |||||  
Db 10 YSKYKAAAAA 20

RESULT 14  
HXD8\_HUMAN STANDARD; PRT; 290 AA.  
AC P13378;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Homeobox protein Hox-D8 (Hox-4E) (Hox-5.4).  
GN Name=HOXD8; Synonyms=HOX4E;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Birren B., Linton L., Nusbaum C., Lander E.,  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kosaki K., Kosaki R., Suzuki T., Yoshihashi H., Sasaki K., Matsuo N.,  
RT "A complete mutation analysis panel of human HOX genes.",  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 193-287 FROM N.A.  
RX MEDLINE=89306602; PubMed=2568311;  
RA Oliver G., Sidel N., Fiske N., Heinzmann C., Mohandas T.,  
RA Sparkes R.S., de Robertis E.M.;  
RT "Complementary homeo protein gradients in developing limb buds.";  
RL Genes Dev. 3:641-650(1989).  
CC -!- FUNCTION: Sequence-specific transcription factor which is part of  
CC a developmental regulatory system that provides cells with  
CC specific positional identities on the anterior-posterior axis.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: Belongs to the Antp homeobox family.  
CC -!- SIMILARITY: Contains 1 homeobox domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use, by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AC009336; -; NOT ANNOTATED\_CDS.  
DR EMBL; AY014304; AAG42152.1; -  
DR EMBL; AY014303; AAG42152.1; JOINED.  
DR EMBL; X15507; CAA33529.1; -.

DR PIR; B32830; B32830.  
DR HSSP; P02833; 9ANT.  
DR TRANSFAC; T03332; -.  
DR Genew; HGNC:5139; HOXD8.  
DR MIM; 142985; -.  
DR GO; GO:0005634; C:nucleus; NAS.  
DR GO; GO:0003700; F:transcription factor activity; NAS.  
DR GO; GO:0008595; P:determination of anterior/posterior axis, e...; NAS.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.  
DR InterPro; IPR001827; Antennapedia.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain\_like.  
DR Pfam; PF00046; Homeobox; 1.  
DR PRINTS; PR00025; ANTENNAPEIDIA.  
DR PRINTS; PR00024; HOMEBOX.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00032; ANTENNAPEIDIA; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
DR Developmental protein; DNA-binding; Homeobox; Nuclear protein;  
KW Transcription regulation.  
KM DOMAIN 15 23 Poly-Ala.  
FT DOMAIN 45 50 Poly-Ala.  
FT DOMAIN 109 123 Poly-Pro.  
FT DNA BIND 197 256 Homeobox.  
FT CONFLICT 287 287 G -> A (in Ref. 3).  
SQ SEQUENCE 290 AA; 31910 MW; 75FF95A73E2A85F CRC64;

Query Match 59.2%; Score 42; DB 1; Length 290;  
Best Local Similarity 81.8%; Pred. No. 1.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAAA 15  
| |||||  
Db 10 YSKYKAAAAA 20

RESULT 15  
Q6AY89 PRELIMINARY; PRT; 364 AA.  
ID Q6AY89;  
AC Q6AY89;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Director MGC Project;  
RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC079147; AAH79147.1; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003697; F:single-stranded DNA binding; IEA.  
DR GO; GO:0030528; F:transcription regulator activity; IEA.  
DR InterPro; IPR006594; LISH.  
DR InterPro; IPR007591; SSDP.  
DR InterPro; IPR008116; SSDP\_DNA\_bind.  
DR Pfam; PF04503; SSDP; 1.  
DR PRINTS; PR01743; SSDNABINDING.  
DR SMART; SM00667; LISH; 1.  
DR PROSITE; PS50896; LISH; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 364 AA; 37518 MW; A31EEB7AC4F58A78 CRC64;  
  
Query Match 59.2%; Score 42; DB 2; Length 364;  
Best Local Similarity 64.3%; Pred. No. 1.4e+02;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Oy 1 EAKKYEAAYKAAAA 14  
|||::|  
Db 85 EAKVFQDYSAAAAA 98

Search completed: April 4, 2005, 17:31:07  
Job time : 114.094 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 16:53:02 ; Search time 132.812 Seconds  
(without alignments)  
49.505 Million cell updates/sec

Title: US-10-056-583A-96  
Perfect score: 83  
Sequence: 1 APEKAKFEAFKAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	17	5	ABP52302 HLA-DR2 m
2	80	96.4	17	5	ABP52303 HLA-DR2 m
3	69	83.1	17	5	ABP52294 HLA-DR2 m
4	69	83.1	19	5	ABP52295 HLA-DR2 m
5	64	77.1	15	5	ABP52301 HLA-DR2 m
6	64	77.1	15	5	ABP52297 HLA-DR2 m
7	61	73.5	15	5	ABP52291 HLA-DR2 m
8	58	69.9	15	5	ABP52271 HLA-DR2 m
9	58	69.9	15	5	ABP52298 HLA-DR2 m
10	58	69.9	15	5	ABP52300 HLA-DR2 m
11	58	69.9	15	5	ABP52304 HLA-DR2 m
12	58	69.9	17	5	ABP52296 HLA-DR2 m
13	57	68.7	15	5	ABP52299 HLA-DR2 m
14	55	66.3	15	5	ABP52290 HLA-DR2 m
15	55	66.3	15	5	ABP52292 HLA-DR2 m
16	52	62.7	15	5	ABP52270 HLA-DR2 m
17	51	61.4	15	5	ABP52305 HLA-DR2 m
18	50	60.2	572	4	ABP59072 Drosophila
19	48	57.8	15	5	ABP52263 HLA-DR2 m
20	47	56.6	15	5	ABP52272 HLA-DR2 m
21	46	55.4	15	5	ABP52259 HLA-DR2 m
22	46	55.4	15	5	ABP52257 HLA-DR2 m
23	46	55.4	203	8	ADP30243 Bacterial
24	46	55.4	465	6	ABU38244 Protein e
25	46	55.4	469	7	ABO79123 Pseudomon

26	45	54.2	15	5	ABP52289 HLA-DR2 m
27	44	53.0	21	2	AAW19062 Trypanoso
28	44	53.0	21	2	AAW19087 Trypanoso
29	44	53.0	21	2	AAV32839 TCE repea
30	44	53.0	21	2	AAV23311 Epitope o
31	44	53.0	21	2	AAV23313 Repeat se
32	44	53.0	21	3	AAV26466 T.cruzi s
33	44	53.0	21	3	AAV26468 T.cruzi s
34	44	53.0	145	3	AAV32749 Eucalyptu
35	44	53.0	262	2	AAV06913 T. cruzi
36	44	53.0	262	2	AAV32848 TCE prote
37	44	53.0	263	2	AAV23306 TCE anti
38	43	51.8	15	5	ABP52253 HLA-DR2 m
39	43	51.8	15	5	ABP52251 HLA-DR2 m
40	43	51.8	15	5	ABP52239 HLA-DR2 m
41	43	51.8	351	6	ABU35314 Protein e
42	43	51.8	397	6	ABO00558 Novel hum
43	43	51.8	1512	7	ADP47702 Human NOV
44	43	51.8	1512	8	ADJ78972 Human NOV
45	42	50.6	15	5	ABP52261 HLA-DR2 m

ALIGNMENTS

RESULT 1  
ABP52302  
ID ABP52302 standard; peptide; 17 AA.  
XX  
AC ABP52302;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:96.  
XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 83; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APEKAKFEAFKAAAPAA 17  
Db 1 APEKAKFEAFKAAAPAA 17  
RESULT 2  
ABP52303  
ID ABP52303 standard; peptide; 17 AA.  
XX  
AC ABP52303;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:97.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX

SQ Sequence 17 AA;  
Query Match 96.4%; Score 80; DB 5; Length 17;  
Best Local Similarity 94.1%; Pred. No. 3.6e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APEKAKFEAFKAAAPAA 17  
Db 1 APEKAKFEAFKAAAPAA 17  
RESULT 3  
ABP52294  
ID ABP52294 standard; peptide; 17 AA.  
XX  
AC ABP52294;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
Query Match 83.1%; Score 69; DB 5; Length 17;  
Best Local Similarity 82.4%; Pred. No. 0.00023;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 APEKAKFEAFKAAAPAA 17

Db 1 APEKAKYEAYKAAAAA 17

RESULT 4

ABP52295 ID ABP52295 standard; peptide; 19 AA.

XX AC ABP52295;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:89.

XX KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

OS Homo sapiens.

XX OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX PT New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to CC ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 19 AA;

Query Match 83.1%; Score 69; DB 5; Length 19;  
Best Local Similarity 82.4%; Pred. No. 0.00026;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
ID 1 APEKAKYEAYKAAAAA 17

RESULT 5  
ABP52301 ID ABP52301 standard; peptide; 15 AA.

XX AC ABP52301;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:95.

XX KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

OS Homo sapiens.

XX OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX PT New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to CC ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 15 AA;

Query Match 77.1%; Score 64; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.0013;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKAKFEAFKAAAPA 17  
ID 1 EKAKFEAFKAAAPA 15

RESULT 6  
ABP52297 ID ABP52297 standard; peptide; 15 AA.

XX AC ABP52297;  
XX DT 16-OCT-2002 (first entry)  
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:91.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; anti-inflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has anti-inflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
CC  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 77.1%; Score 64; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0013;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 3 EKAKFEAFKAAAPAA 17  
|||:|||||  
Db 1 EKPKFEAYKAAAPAA 15  
RESULT 7  
ABP52291  
ID ABP52291 standard; peptide; 15 AA.  
XX  
AC ABP52291;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:85.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; anti-inflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has anti-inflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
CC  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 73.5%; Score 61; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.0042;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 3 EKAKFEAFKAAAPAA 17  
|||:|||||  
Db 1 EKPKFEAYKAAAPAA 15  
RESULT 8  
ABP52271  
ID ABP52271 standard; peptide; 15 AA.  
XX  
AC ABP52271;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; anti-inflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX

PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
OY  
Query Match 69.9%; Score 58; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.013;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Db 3 EKAKEFAFKAAAPAA 17  
1 EKAKEYEAYKAAAAA 15  
RESULT 9  
ABP52298  
ID ABP52298 standard; peptide; 15 AA.  
XX  
AC ABP52298;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:92.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;

XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
OY  
Query Match 69.9%; Score 58; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.013;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Db 3 EKAKEFAFKAAAPAA 17  
1 EKAKEYEAYKAAAAA 15  
RESULT 10  
ABP52300  
ID ABP52300 standard; peptide; 15 AA.  
XX  
AC ABP52300;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:94.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

XX  
PS Claim 28; Page 39; 54pp; English..

AA The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

**SQ Sequence 15 AA;**

Query Match	69.9%	Score 58;	DB 5;	Length 15;
Best Local Similarity	86.7%	Pred. No. 0.013;		
Matches 13; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	3	EKAKFEAFKAAAPR	17
Dd	1	EKPKEEAFKAAAPR	15

RESULT 11  
ABP52304

ID ABP52304 standard; peptide; 15 AA.

AC ABP52304;

DT 16-OCT-2002 (first entry)

DE	HLA-DR2 molecule binding peptide SEQ ID NO:98.
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
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98	98
99	99
100	100

Human leukocyte antigen, HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

OS	Homo sapiens.
OS	Synthetic.
OS	

PN WO200259143-A2.

01-AUG-2002. PD

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

aa New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DQ protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

aa The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
CC  
CC  
SQ Sequence 15 AA;

Sequence 15 AA:

Query Match	69.9%	Score 58	DB 5	Length 15
Best Local Similarity	80.0%	Pred. No. 0.013		
Matches 12; Conservative	1	Mismatches	2	Indels 0; Gaps 0

Qy		3	EKAKFEAFKAAPA	17
			:	
Db		1	EAPKFEAYKAAAPA	15

RESULT 12  
ABP52296

ID ABP52296 standard; peptide; 17 AA.

AC ABP52296;

DT 16-OCT-2002 (first entry)

DE	HLA-DR2 molecule binding peptide SEQ ID NO:90.
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
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14	14
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169	169
170	170
171	

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; anti-inflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS	Homo sapiens.
OS	Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

...  
PA (HARD ) HARVARD COLLEGE.

Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

AA New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-D2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to



CC ABP52305 represent peptides used in the exemplification of the present  
XX invention  
SQ Sequence 17 AA;

Query Match 69.9%; Score 58; DB 5; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.015;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 EKAKFEAFKAAAPAA 17  
|||:|:|:|:|:|  
DB 1 EKAKYEAYKAAAPAA 15

## RESULT 13

ABP52299  
ID ABP52299 standard; peptide; 15 AA.

XX ABP52299;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:93.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.

OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

SQ Sequence 15 AA;

Query Match 68.7%; Score 57; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.019;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 EKAKFEAFKAAAPAA 17  
|||:|:|:|:|:|  
DB 1 EKPKVEAYKAAAPAA 15

## RESULT 14

ABP52290  
ID ABP52290 standard; peptide; 15 AA.

XX ABP52290;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:84.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.

OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

SQ Sequence 15 AA;

Query Match 66.3%; Score 55; DB 5; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.04;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 EKAKFEAFKAAAPAA 17  
|||:|:|:|:|:|  
DB 1 EAPKYEAYKAAAPAA 15

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RESULT 15
ABP52292
ID ABP52292 standard; peptide; 15 AA.
XX
AC ABP52292;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:86.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

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Query Match 66.3%; Score 55; DB 5; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 3 EKAKFEAFKAAAPPA 17
   | :||:|||||
Db 1 EAPKYEAYKAAAPPA 15

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Search completed: April 4, 2005, 17:26:04  
Job time : 133.812 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:27:14 ; Search time 31.3438 Seconds  
(without alignments)  
40.488 Million cell updates/sec

Title: US-10-056-583A-96  
Perfect score: 83  
Sequence: 1 APEKAKEAFKAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	55.4	212	4 US-09-902-540-16451	Sequence 16451, A
2	46	55.4	469	4 US-09-252-991A-27869	Sequence 27869, A
3	44	53.0	21	2 US-08-557-309B-58	Sequence 58, Appl
4	44	53.0	21	2 US-08-929-414-11	Sequence 11, Appl
5	44	53.0	21	3 US-08-834-306-56	Sequence 56, Appl
6	44	53.0	21	3 US-08-834-306-58	Sequence 58, Appl
7	44	53.0	21	3 US-08-993-674A-56	Sequence 58, Appl
8	44	53.0	21	3 US-08-993-674A-58	Sequence 58, Appl
9	44	53.0	21	4 US-09-256-976-56	Sequence 56, Appl
10	44	53.0	21	4 US-09-256-976-58	Sequence 58, Appl
11	44	53.0	145	4 US-09-640-211A-798	Sequence 798, Appl
12	44	53.0	262	1 US-08-403-379A-1	Sequence 1, Appl
13	44	53.0	262	2 US-08-929-414-1	Sequence 1, Appl
14	44	53.0	263	2 US-08-557-309B-51	Sequence 51, Appl
15	44	53.0	263	3 US-08-834-306-51	Sequence 51, Appl
16	44	53.0	263	3 US-08-993-674A-51	Sequence 51, Appl
17	44	53.0	162	4 US-09-256-976-51	Sequence 51, Appl
18	42	50.6	162	4 US-09-732-210-1445	Sequence 1445, Ap
19	42	50.6	324	4 US-09-248-796A-17156	Sequence 17156, A
20	41	49.4	21	2 US-08-557-309B-61	Sequence 61, Appl
21	41	49.4	21	2 US-08-929-414-13	Sequence 13, Appl
22	41	49.4	21	3 US-08-834-306-60	Sequence 60, Appl
23	41	49.4	21	3 US-08-993-674A-60	Sequence 60, Appl
24	41	49.4	21	4 US-09-256-976-60	Sequence 60, Appl
25	41	49.4	642	4 US-09-489-039A-12434	Sequence 12434, A
26	40	48.2	21	1 US-08-403-379A-3	Sequence 3, Appl
27	40	48.2	21	2 US-08-557-309B-52	Sequence 52, Appl

28	40	48.2	21	2 US-08-557-309B-57	Sequence 57, Appl
29	40	48.2	21	2 US-08-557-309B-60	Sequence 60, Appl
30	40	48.2	21	2 US-08-929-414-3	Sequence 3, Appl
31	40	48.2	21	2 US-08-929-414-10	Sequence 10, Appl
32	40	48.2	21	2 US-08-929-414-12	Sequence 12, Appl
33	40	48.2	21	3 US-08-834-306-55	Sequence 55, Appl
34	40	48.2	21	3 US-08-834-306-59	Sequence 59, Appl
35	40	48.2	21	3 US-08-993-674A-55	Sequence 55, Appl
36	40	48.2	21	3 US-08-993-674A-59	Sequence 59, Appl
37	40	48.2	21	3 US-09-248-588-46	Sequence 46, Appl
38	40	48.2	21	4 US-09-256-976-55	Sequence 55, Appl
39	40	48.2	21	4 US-09-256-976-59	Sequence 59, Appl
40	40	48.2	85	4 US-09-256-976-82	Sequence 82, Appl
41	40	48.2	94	4 US-09-256-976-95	Sequence 95, Appl
42	40	48.2	214	4 US-09-252-991A-31304	Sequence 31304, A
43	40	48.2	219	2 US-08-557-309B-54	Sequence 54, Appl
44	40	48.2	419	4 US-09-489-039A-13260	Sequence 13260, A
45	40	48.2	442	3 US-08-834-306-52	Sequence 52, Appl

## ALIGNMENTS

```
RESULT 1
US-09-902-540-16451
; Sequence 16451, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16451
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16451

Query Match          55.4%; Score 46; DB 4; Length 212;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 PEKAKEAFKAAAP 16
Db      134 PDQAPFDALIAAAP 148

RESULT 2
US-09-252-991A-27869
; Sequence 27869, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27869
; LENGTH: 469
; TYPE: PRT
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ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27869

Query Match 55.4%; Score 46; DB 4; Length 469;  
Best Local Similarity 62.5%; Pred. No. 11;  
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 PEKAKFEAFKAAAPA 17  
DB 176 PNALAFERFKAAYPA 191

RESULT 3  
US-08-557-309B-58

Sequence 58, Application US/08557309B  
Patent No. 5916572

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/557,309B

FILING DATE: 14-NOV-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.422

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-557-309B-58

Query Match 53.0%; Score 44; DB 2; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.78;

Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFKFAKAAAPA 17  
DB 5 APAKAAAPAKAAAPA 21

RESULT 4

US-08-929-414-11

Sequence 11, Application US/08929414

Patent No. 5942403

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Haughton, Raymond

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION

TITLE OF INVENTION: OF T. CRUZI INFECTION

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/929,414

FILING DATE: 15-SEP-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.406C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-929-414-11

Query Match 53.0%; Score 44; DB 2; Length 21;

Best Local Similarity 64.7%; Pred. No. 0.78;

Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFKFAKAAAPA 17  
DB 5 APAKAAAPAKAAAPA 21

RESULT 5

US-08-834-306-56

Sequence 56, Application US/08834306

Patent No. 6054135

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,306

FILING DATE: 15-APR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.422C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-834-306-56

Query Match 53.0%; Score 44; DB 3; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.78;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFKFAKAAAPA 17  
||| |||||  
Db 5 APAKAAAPAKAAAPA 21

## RESULT 6

US-08-834-306-58  
; Sequence 58, Application US/08834306  
; Patent No. 6054135  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Houghton, Raymond L.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,306  
; FILING DATE: 15-APR-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.422C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-834-306-58

Query Match 53.0%; Score 44; DB 3; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.78;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFKFAKAAAPA 17  
||| |||||  
Db 5 APAKAAAPAKAAAPA 21

## RESULT 7

US-08-993-674A-56  
; Sequence 56, Application US/08993674A

Patent No. 6228372  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Smith, John M.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/993,674A  
; FILING DATE: 18-DEC-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.422C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-993-674A-56

Query Match 53.0%; Score 44; DB 3; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.78;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFKFAKAAAPA 17  
||| |||||  
Db 5 APAKAAAPAKAAAPA 21

## RESULT 8

US-08-993-674A-58  
; Sequence 58, Application US/08993674A  
; Patent No. 6228372  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Smith, John M.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,674A  
FILING DATE: 18-DEC-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.422C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-993-674A-58

Query Match 53.0%; Score 44; DB 3; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.78;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
||| |||||  
Db 5 APAKAAAPAKAAAPA 21

## RESULT 9

US-09-256-976-56  
Sequence 56, Application US/09256976  
Patent No. 6419933  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Smith, John M.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION  
TITLE OF INVENTION: OF T. CRUZI INFECTION  
FILE REFERENCE: 210121.422C3  
CURRENT APPLICATION NUMBER: US/09/256,976  
CURRENT FILING DATE: 1999-02-24  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 56  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: TCE antigenic  
US-09-256-976-56

Query Match 53.0%; Score 44; DB 4; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.78;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
||| |||||  
Db 5 APAKAAAPAKAAAPA 21

## RESULT 10

US-09-256-976-58  
Sequence 58, Application US/09256976  
Patent No. 6419933  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Lodes, Michael J.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Smith, John M.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION  
TITLE OF INVENTION: OF T. CRUZI INFECTION  
FILE REFERENCE: 210121.422C3  
CURRENT APPLICATION NUMBER: US/09/256,976  
CURRENT FILING DATE: 1999-02-24  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 58  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: TCE  
US-09-256-976-58

Query Match 53.0%; Score 44; DB 4; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.78;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
||| |||||  
Db 5 APAKAAAPAKAAAPA 21

## RESULT 11

US-09-640-211A-798  
Sequence 798, Application US/09640211A  
Patent No. 6833446  
GENERAL INFORMATION:  
APPLICANT: Wood, Marion  
APPLICANT: Shenk, Michael A.  
APPLICANT: McGrath, Annette  
APPLICANT: Glenn, Matthew  
TITLE OF INVENTION: Modifications and Methods for the  
TITLE OF INVENTION: Modification of Gene Transcription  
FILE REFERENCE: 11000.1021C1U  
CURRENT APPLICATION NUMBER: US/09/640,211A  
CURRENT FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 2368  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 798  
LENGTH: 145  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-09-640-211A-798

Query Match 53.0%; Score 44; DB 4; Length 145;  
Best Local Similarity 64.7%; Pred. No. 6.4;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
||| |||||  
Db 113 AP1PASFSAPSAAAPA 129

## RESULT 12

US-08-403-379A-1  
Sequence 1, Application US/08403379A  
Patent No. 5756662  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION  
TITLE OF INVENTION: OF T. CRUZI INFECTION  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle

STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,379A  
FILING DATE: 14-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 262 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-403-379A-1

Query Match 53.0%; Score 44; DB 1; Length 262;  
Best Local Similarity 64.7%; Pred. No. 12;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
|||  
Db 141 APAKAAAPAKAAAPA 157

## RESULT 13

US-08-929-414-1  
Sequence 1, Application US/08929414  
Patent No. 5942403  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Haughton, Raymond  
APPLICANT: Skeiky, Yasir A.W.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION  
TITLE OF INVENTION: OF T. CRUZI INFECTION  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/929,414  
FILING DATE: 15-SEP-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.406C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 262 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-929-414-1

Query Match 53.0%; Score 44; DB 2; Length 262;  
Best Local Similarity 64.7%; Pred. No. 12;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
|||  
Db 141 APAKAAAPAKAAAPA 157

## RESULT 14

US-08-557-309B-51  
Sequence 51, Application US/08557309B  
Patent No. 5916572  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Haughton, Raymond L.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/557,309B  
FILING DATE: 14-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.422  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-557-309B-51

Query Match 53.0%; Score 44; DB 2; Length 263;  
Best Local Similarity 64.7%; Pred. No. 12;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
|||  
Db 142 APAKAAAPAKAAAPA 158

## RESULT 15

US-08-834-306-51  
Sequence 51, Application US/08834306  
Patent No. 6054135  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/834,306  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.422C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-834-306-51

Query Match 53.0%; Score 44; DB 3; Length 263;  
Best Local Similarity 64.7%; Pred. No. 12;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
Db 142 APAKAAAAPAKAAAPA 158

Search completed: April 4, 2005, 17:47:40  
Job time : 32.3438 secs

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OM protein - protein search, using sw model

Run on: April 4, 2005, 17:21:54 ; Search time 100.406 Seconds  
(without alignments)  
56.143 Million cell updates/sec

Title: US-10-056-583A-96  
Perfect score: 83  
Sequence: 1 APEKAKFEAFKAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	14	US-10-056-583-96 Sequence 96, Appl
2	80	96.4	17	14	US-10-056-583-97 Sequence 97, Appl
3	69	83.1	17	14	US-10-056-583-88 Sequence 88, Appl
4	69	83.1	19	14	US-10-056-583-89 Sequence 89, Appl
5	64	77.1	15	14	US-10-056-583-91 Sequence 91, Appl
6	64	77.1	15	14	US-10-056-583-95 Sequence 95, Appl
7	61	73.5	15	14	US-10-056-583-85 Sequence 85, Appl
8	58	69.9	15	14	US-10-056-583-65 Sequence 65, Appl
9	58	69.9	15	14	US-10-056-583-94 Sequence 94, Appl
10	58	69.9	15	14	US-10-056-583-98 Sequence 98, Appl
11	58	69.9	17	14	US-10-056-583-90 Sequence 90, Appl
12	57	68.7	15	14	US-10-056-583-93 Sequence 93, Appl
13	55	66.3	15	14	US-10-056-583-84 Sequence 84, Appl

14	55	66.3	15	14	US-10-056-583-86	Sequence 86, Appl
15	52	62.7	15	14	US-10-056-583-64	Sequence 64, Appl
16	52	62.7	15	14	US-10-056-583-92	Sequence 92, Appl
17	51	61.4	15	14	US-10-056-583-99	Sequence 99, Appl
18	48	57.8	15	14	US-10-056-583-57	Sequence 57, Appl
19	47	56.6	15	14	US-10-056-583-66	Sequence 66, Appl
20	46	55.4	15	14	US-10-056-583-51	Sequence 51, Appl
21	46	55.4	15	14	US-10-056-583-53	Sequence 53, Appl
22	46	55.4	203	15	US-10-369-493-19276	Sequence 19276, A
23	46	55.4	465	15	US-10-282-122A-66168	Sequence 66168, A
24	45	54.2	15	14	US-10-056-583-83	Sequence 83, Appl
25	44	53.0	113	15	US-10-425-114-70689	Sequence 70689, A
26	44	53.0	386	16	US-10-437-963-194029	Sequence 194029, A
27	43	51.8	15	14	US-10-056-583-33	Sequence 33, Appl
28	43	51.8	15	14	US-10-056-583-45	Sequence 45, Appl
29	43	51.8	15	14	US-10-056-583-47	Sequence 47, Appl
30	43	51.8	121	16	US-10-767-701-49020	Sequence 49020, A
31	43	51.8	351	15	US-10-282-122A-63238	Sequence 63238, A
32	43	51.8	397	15	US-10-243-552-360	Sequence 360, Appl
33	43	51.8	1512	15	US-10-210-130-64	Sequence 64, Appl
34	42	50.6	15	14	US-10-056-583-38	Sequence 38, Appl
35	42	50.6	15	14	US-10-056-583-55	Sequence 55, Appl
36	42	50.6	15	14	US-10-056-583-56	Sequence 56, Appl
37	42	50.6	15	14	US-10-056-583-63	Sequence 63, Appl
38	42	50.6	162	15	US-10-282-122A-62570	Sequence 62570, A
39	42	50.6	162	15	US-10-282-122A-64801	Sequence 64801, A
40	42	50.6	180	15	US-10-424-599-266399	Sequence 266399, A
41	42	50.6	421	15	US-10-282-122A-56483	Sequence 56483, A
42	42	50.6	570	15	US-10-094-749-3117	Sequence 3117, Ap
43	42	50.6	570	16	US-10-408-765A-2514	Sequence 2514, Ap
44	41.5	50.0	307	16	US-10-469-061A-45	Sequence 45, Appl
45	41.5	50.0	307	16	US-10-469-061A-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1  
US-10-056-583-96  
; Sequence 96, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THEAPEPTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056, 583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263, 569  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-96

Query Match 100.0%; Score 83; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.8e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
Db 1 APEKAKFEAFKAAAPA 17

RESULT 2  
US-10-056-583-97



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; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

Query Match          96.4%; Score 80; DB 14; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 APEKAKFEAFKAAAPAA 17
Db      1 APEKAKFEAYKAAAPAA 17

RESULT 3
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

Query Match          83.1%; Score 69; DB 14; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 APEKAKFEAFKAAAPAA 17
Db      1 APEKAKFEAYKAAAPAA 17

RESULT 4
US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89

Query Match          83.1%; Score 69; DB 14; Length 19;
Best Local Similarity 82.4%; Pred. No. 0.00014;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 APEKAKFEAFKAAAPAA 17
Db      1 APEKAKFEAYKAAAPAA 17

RESULT 5
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91

Query Match          77.1%; Score 64; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00071;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 EKAKFEAFKAAAPAA 17
Db      1 EKPKFEAYKAAAPAA 15

RESULT 6
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```



```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95
```

```
Query Match          77.1%; Score 64; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      3 EKAKFEAFKAAAPAA 17
        |||:|||||
Db      1 EKAKFEAFKAAAPAA 15
```

## RESULT 7

```
US-10-056-583-85
; Sequence 85, Application US/10055583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85
```

```
Query Match          73.5%; Score 61; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0022;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      3 EKAKFEAFKAAAPAA 17
        |||:|||||
Db      1 EKPKYEAYKAAAPAA 15
```

## RESULT 8

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US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
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```
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65
```

```
Query Match          69.9%; Score 58; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.007;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      3 EKAKFEAFKAAAPAA 17
        |||:|||||
Db      1 EKAKYEAYKAAAPAA 15
```

## RESULT 9

```
US-10-056-583-94
; Sequence 94, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-94
```

```
Query Match          69.9%; Score 58; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      3 EKAKFEAFKAAAPAA 17
        |||:|||||
Db      1 EKPKFEAFKAAAPAA 15
```

## RESULT 10

```
US-10-056-583-98
; Sequence 98, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-98

Query Match 69.9%; Score 58; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.007;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAFKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EAPKFEAYKAAAPAA 15

RESULT 11  
US-10-056-583-90

Sequence 90, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 90  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-90

Query Match 69.9%; Score 58; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.0081;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKAKFEAFKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EAKYEAYKAAAPAA 15

RESULT 12

US-10-056-583-93  
Sequence 93, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 93  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-93

Query Match 68.7%; Score 57; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.01;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAFKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EKPVEAYKAAAPAA 15

RESULT 13

US-10-056-583-84  
Sequence 84, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 84  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-84

Query Match 66.3%; Score 55; DB 14; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.022;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAFKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EAPKFEAYKAAAPAA 15

RESULT 14

US-10-056-583-86  
Sequence 86, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 86  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-86

Query Match 66.3%; Score 55; DB 14; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.022;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAFKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EAPKFEAYKAAAPAA 15

RESULT 15  
US-10-056-583-64

; Sequence 64, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 64  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-64

Query Match 62.7%; Score 52; DB 14; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.069;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAFKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
DB 1 EAKYEAYKAAAAAA 15

Search completed: April 4, 2005, 17:34:53  
Job time : 101.406 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

```
Run on:      April 4, 2005, 17:01:24 ; Search time 28.1562 Seconds
              (without alignments)
              58.093 Million cell updates/sec
```

Title:	US-10-056-583A-96
Perfect score:	83
Sequence:	1 APEKAKFEAFKAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
1: pir_79:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	57.8	389	2	G87332	hypothetical prote
2	46	55.4	465	2	D83598	probable zinc prote
3	45.5	54.8	189	2	S77930	exoskeletal protei
4	45.5	54.8	189	2	S77935	exoskeletal protei
5	45	54.2	179	2	F97683	50S ribosomal prot
6	45	54.2	179	2	AF2908	50S ribosomal prot
7	44	53.0	97	2	G60110	repetitive protein
8	44	53.0	408	2	AH3269	50S ribosomal prot
9	43	51.8	128	2	T40464	probable RNA bindi
10	42	50.6	84	2	T23177	hypothetical prote
11	42	50.6	162	2	H70927	probable rpsf prot
12	42	50.6	421	2	JV0057	cola protein - Escs
13	42	50.6	743	2	F71062	hypothetical protee
14	41	49.4	405	2	AH2752	dihydrolipoamide S
15	41	49.4	447	2	AB3359	dihydrolipoamide S
16	41	49.4	457	2	F97533	dihydrolipoamide a
17	41	49.4	565	2	C87278	hypothetical prote
18	41	49.4	629	2	AH0521	dihydrolipoamide a
19	41	49.4	828	2	F96535	hypothetical prote
20	40	48.2	73	2	S40015	phd protein - phag
21	40	48.2	136	2	AI0026	50S ribosomal prob
22	40	48.2	143	2	A87678	hypothetical protee
23	40	48.2	306	2	G96014	hypothetical protee
24	40	48.2	321	2	T07922	probable l-aminocy
25	40	48.2	416	2	AB1609	branched-chain alp
26	40	48.2	507	1	NNBY1	anthranilate synth
27	40	48.2	704	2	B83914	beta-xylosidase (1
28	40	48.2	1020	1	QF0UH	neurofilament trip
29	40	48.2	1132	2	C75259	probable iron-sulf

30	39	47.0	106	2	A81203	conserved hypot
31	39	47.0	117	2	C81779	hypothetical prote
32	39	47.0	129	1	TN1JG3	trans-activating t
33	39	47.0	136	1	R5EC16	ribosomal protein
34	39	47.0	136	2	AH1006	50S ribosomal chai
35	39	47.0	136	2	F85996	50S ribosomal subu
36	39	47.0	136	2	B91151	50S ribosomal subu
37	39	47.0	151	1	HSMT2A	histone H2A.2 - wh
38	39	47.0	184	2	D83234	hypothetical prote
39	39	47.0	196	2	E97352	transcription regu
40	39	47.0	198	2	A12622	conserved hypot
41	39	47.0	217	2	A97405	hypothetical prote
42	39	47.0	329	2	D96030	hypothetical prote
43	39	47.0	338	2	T36785	hypothetical prote
44	39	47.0	347	2	A81794	probable rotamase
45	39	47.0	348	2	B81216	peptidyl-prolyl ci

## ALIGNMENTS

RESULT 1  
G87332  
hypothetical protein CC0674 [imported] - *Caulobacter crescentus*  
C/Species: *Caulobacter crescentus*  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C/Accession: G87332  
R/Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo-  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A/Title: Complete Genome Sequence of *Caulobacter crescentus*.  
A/Reference number: A87249; MUID:21173698; PMID:11259647  
A/Accession: G87332  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-389 <STO>  
A/Cross-references: UNIPROT:Q9AAC8; GB:AE005673; NID:g13421893; PIDN:AAK22659.1; GSPDB:..  
C/Genetics:  
A/Gene: CC0674

Query Match	57.8%	Score 48;	DB 2;	Length 389;
Best Local Similarity	64.7%;	Pred. No. 3;		
Matches 11; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY 1 APEKAKFEAFKAAAAPA 17  
| | | | | | | |  
Db 63 ADGKTSVETFKAAAAPA 79

RESULT 2  
D83598  
probable zinc proteinase PA0372 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C:Species: *Pseudomonas aeruginosa*  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C;Accession: D83598

R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim

..; LORY, S.; OLSON, M.V.  
NATURE 105 050 054 2000

**A+Title:** Complete genome sequence of *Pseudomonas aeruginosa* PA01 - an opportunistic pathogen  
**NALC#** 408, 933-964, 2000

A:Reference number: A82950: MUID:20437337: PMID:10984043

A: Accession: D83598

A;Status: prelimina

A;molecule type: DNA

A;Residues: 1-465 <STO>

A; Cross-references: UNL

C:Genetics:  
M;Experimental source: Brian Fowl

A:Gene: PA0372

**SECRET**

Query Match	55.4%;	Score 46;	DB 2;	Length 465;
Best Local Similarity	62.5%;	Pred. NO. 7.6;		

**Page 1**

Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2 PEKAKFEAFKAAAPA 17  
| | | | | | | | | |  
Db 172 PNALAFERFKAAAYPA 187

## RESULT 3

S77930  
exoskeletal protein HACP202A - American lobster (fragment)  
C:Species: Homarus americanus (American lobster)  
C:Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S77930  
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.  
submitted to the Protein Sequence Database, June 1997  
A:Description: Characterization of exoskeletal proteins from the American lobster, Homarus  
A:Reference number: S77925  
A:Accession: S77930  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-189 <NOU>  
A:Cross-references: UNIPROT:Q7M496

Query Match 54.8%; Score 45.5; DB 2; Length 189;  
Best Local Similarity 66.7%; Pred. No. 3.8;  
Matches 12; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 APEKAKFEAFKAAAPA 17  
| | | | | | | | | |  
Db 9 AAEKARFFQAFKAAEAAA 26

## RESULT 4

S77935  
exoskeletal protein HACP202B - American lobster (fragment)  
C:Species: Homarus americanus (American lobster)  
C:Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S77935  
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.  
submitted to the Protein Sequence Database, June 1997  
A:Description: Characterization of exoskeletal proteins from the American lobster, Homarus  
A:Reference number: S77925  
A:Accession: S77935  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-189 <NOU>  
A:Cross-references: UNIPROT:Q7M495

Query Match 54.8%; Score 45.5; DB 2; Length 189;  
Best Local Similarity 66.7%; Pred. No. 3.8;  
Matches 12; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 APEKAKFEAFKAAAPA 17  
| | | | | | | | | |  
Db 9 AAEKARFFQAFKAAEAAA 26

## RESULT 5

F97683  
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: F97683  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A:Reference number: A97559; MUID:21608551; PMID:11743194  
A:Accession: F97683  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-179 <KUR>  
A:Cross-references: UNIPROT:Q8UBZ5; GB:AE007669; PIDN:AAK8423.1; PID:g15157917; GSPDB:G

C:Genetics:  
A:Gene: AGR\_C 4900  
A:Map position: circular chromosome  
C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 54.2%; Score 45; DB 2; Length 179;  
Best Local Similarity 64.7%; Pred. No. 4.4;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
| | | | | | | | | |  
Db 135 ABEKARLEAEKVAQA 151

## RESULT 6

AF2908  
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AF2908  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, P.; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, M.; E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AF2908  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-179 <KUR>  
A:Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:g17741210; GSPDB:G  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: rplS  
A:Map position: circular chromosome  
C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 54.2%; Score 45; DB 2; Length 179;  
Best Local Similarity 64.7%; Pred. No. 4.4;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
| | | | | | | | | |  
Db 135 ABEKARLEAEKVAQA 151

## RESULT 7

G60110  
repetitive protein antigen 69/70 - Trypanosoma cruzi (fragment)  
C:Species: Trypanosoma cruzi  
C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 09-Jul-2004  
C:Accession: G60110  
R:Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E  
Infect. Immun. 57, 1959-1967, 1989  
A:Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.  
A:Reference number: A60110; MUID:89277508; PMID:2659529  
A:Accession: G60110  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-97 <HOF>  
A:Cross-references: UNIPROT:Q7M3W1  
C:Superfamily: varicella-zoster virus gene 22 protein  
C:Keywords: tandem repeat  
F:1-85/Region: 7-residue repeats

Query Match 53.0%; Score 44; DB 2; Length 97;  
Best Local Similarity 64.7%; Pred. No. 3.5;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
| | | | | | | | | |

Db 2 APAKAAAPAKAAAP 18

## RESULT 8

AH3269

dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) [imported] - Brucella melitensis (S

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004

C;Accession: AH3269

R;Delvecchio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens

A;Reference number: AD3252; PMID:11756688

A;Accession: AH3269

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-408 <KUR>

A;Cross-references: UNIPROT:Q9L6H8; GB:AE008917; PIDN:AAU51323.1; PID:g17982020; GSPDB:G

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BMEI0141

A;Map position: 1

C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology

C;Keywords: acyltransferase; coenzyme A

Query Match 53.0%; Score 44; DB 2; Length 408;  
Best Local Similarity 64.7%; Pred. No. 14;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APEKAFEAFAKAAAPA 17

Db 86 APAQKKEAKPAAAPA 102

## RESULT 9

T40464

probable RNA binding protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T40464

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.

submitted to the EMBL Data Library, November 1998

A;Reference number: Z21931

A;Accession: T40464

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-128 <LYN>

A;Cross-references: UNIPROT:O94359; EMBL:AL034382; PIDN:CAA22287.1; GSPDB:GN00067; SPDB:

A;Experimental source: strain 972h-; cosmid c428

C;Genetics:

A;Gene: SPDB:SPBC428.12c

A;Map position: 2

A;introns: 55/1; 108/1

Query Match 51.8%; Score 43; DB 2; Length 128;  
Best Local Similarity 46.7%; Pred. No. 6.7;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PEKAKFEAFKAAAP 16

Db 112 PESADFTFKSTSTP 126

## RESULT 10

T23177

hypothetical protein K01D12.7 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T23177; T23188

R;Dobson, R.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z19703

A;Accession: T23177

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-84 <WIL>

A;Cross-references: UNIPROT:Q27223; UNIPROT:O95QD3; EMBL:Z75543; PIDN:CAA99866.1; GSPDB

A;Experimental source: clone K01D12

A;Accession: T23188

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-84 <W12>

A;Cross-references: EMBL:Z75543; PIDN:CAA99878.1; GSPDB:GN00023; CESP:K01D12.15

A;Experimental source: clone K01D12

C;Genetics:

A;Gene: CESP:K01D12.7; CESP:K01D12.15

A;Map position: 5

Query Match 50.6%; Score 42; DB 2; Length 84;  
Best Local Similarity 62.5%; Pred. No. 6.5;  
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 PEKAKFEAFKAAAPA 17

Db 34 PPKASASATKAAAPA 49

## RESULT 11

H70927

probable rpsP protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C;Accession: H70927

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,

.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: H70927

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-162 <COL>

A;Cross-references: UNIPROT:Q10795; GB:Z74024; GB:AL123456; NID:G3250700; PIDN:CAA98346

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: rpsP

Query Match 50.6%; Score 42; DB 2; Length 162;  
Best Local Similarity 52.9%; Pred. No. 12;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APEKAFEAFAKAAAPA 17

Db 97 APKPSKLEVENAALAAA 113

## RESULT 12

JV0057

tolA protein - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C;Accession: JV0057; B64810

R;Levengood, S.K.; Webster, R.E.

J. Bacteriol. 171, 6600-6609, 1989

A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their prod

A;Reference number: JV0057; MUID:90078104; PMID:2687247

A;Accession: JV0057

A;Molecule type: DNA

A;Residues: 1-421 <LEV>

A;Cross-references: UNIPROT:P19934; GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g14801

A;Experimental source: strain JM105

A;Note: the authors translated the initiation codon GTG for residue 1 as Val

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 17:02:08 ; Search time 125.906 Seconds  
(without alignments)  
69.141 Million cell updates/sec

Title: US-10-056-583A-96  
Perfect score: 83  
Sequence: 1 APEKARFAFKAAAPPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	50	60.2	574	2	Q8SXM8 drosophila
2	50	60.2	607	2	Q9W327 drosophila
3	48	57.8	389	2	Q9AAC8 caulobacter
4	46	55.4	465	2	Q916C2 pseudomonas
5	45.5	54.8	189	2	Q7M495 homarus ame
6	45.5	54.8	189	2	Q7M496 homarus ame
7	45	54.2	179	1	R119_AGR15
8	45	54.2	183	2	Q81W24 bacillus ame
9	45	54.2	607	2	Q8BGF8 xanthomonas
10	45	54.2	836	2	Q8PSL8 methanobact
11	44	53.0	97	2	Q7M3W1 trypanosoma
12	44	53.0	353	2	Q87H28 vibrio para
13	44	53.0	390	2	O85598 brucella ab
14	44	53.0	408	2	Q8FYF8 brucella su
15	44	53.0	408	2	Q916H8 brucella me
16	44	53.0	593	2	Q6AQK4 desulfotale
17	43.5	52.4	306	2	Q7XJ35 medicago tr
18	43	51.8	116	2	Q94359 schizosacch
19	43	51.8	151	2	Q95267 osteretigia
20	43	51.8	174	2	Q73FJ2 bacillus ce
21	43	51.8	250	2	Q7NM09 chromobacte
22	43	51.8	677	2	Q62E59 burkholderi
23	43	51.8	677	2	Q63J18 burkholderi
24	42.5	51.2	300	2	Q729M4 desulfovibr
25	42	50.6	87	2	Q8TUG9 mechanosarc
26	42	50.6	162	1	RS16_MYCBO
27	42	50.6	162	1	RS16_MYCTU
28	42	50.6	177	1	RL19_RHIME
29	42	50.6	181	1	RL19_RHIL0
30	42	50.6	273	2	Q72CN6 desulfovibr
31	42	50.6	413	2	Q83SA1 shigella fl

32	42	50.6	421	1	TOLA ECOLI	P19934 escherichia
33	42	50.6	421	2	Q8FJT1	Q8fjt1 escherichia
34	42	50.6	570	2	Q96M46	Q96m46 homo sapien
35	42	50.6	707	2	Q64CP3	Q64cp3 uncultured
36	42	50.6	743	2	O58900	O58900 pyrococcus
37	41.5	50.0	307	2	Q9M523	Q9m523 tsuga heter
38	41.5	50.0	458	2	Q9M524	Q9m524 tsuga heter
39	41.5	50.0	458	2	Q7SDS7	Q7sds7 neurospora
40	41.5	50.0	629	2	Q8XNK8	Q8xnk8 clostridium
41	41	49.4	114	2	O85393	O85393 coxiella bu
42	41	49.4	145	2	Q7Y3M5	Q7y3m5 enterobacte
43	41	49.4	183	2	Q63HF5	Q63hf5 bacillus ce
44	41	49.4	183	2	Q6HPZ7	Q6hpz7 bacillus th
45	41	49.4	240	2	Q83BL1	Q83bl1 coxiella bu

## ALIGNMENTS

RESULT 1  
Q8SXM8 PRELIMINARY; PRT; 574 AA.  
ID Q8SXM8;  
AC Q8SXM8;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE LD23509P (CG12141-PA).  
GN Name=Aats-1ys; ORFNames=CG12141;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkley;  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celniker S.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abriel J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
RT *melanogaster* euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
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RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirska R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomic perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
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RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
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RG FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.  
DR EMBL; AY089547; AAL90285.1; -  
DR EMBL; AE003447; AAN09255.1; -  
DR HSSP; P13030; 1BBW.  
DR FlyBase; FBgn0027084; Aats-lys.  
DR GO; GO:0005737; C:cytoplasm; IEA.  
DR GO; GO:0004815; F:aspartate-tRNA ligase activity; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0004824; F:lysine-tRNA ligase activity; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0006430; F:aspartyl-tRNA aminoacylation; IEA.  
DR GO; GO:0006412; F:protein biosynthesis; IEA.  
DR InterPro; IPR008994; Nucleic\_acid\_OB.  
DR InterPro; IPR004364; tRNA-synt\_2.  
DR InterPro; IPR00312; tRNA-synt\_2.  
DR InterPro; IPR00313; tRNA-synt\_lys\_2.  
DR InterPro; IPR004365; tRNA-anti.  
DR InterPro; IPR006195; tRNA\_ligase\_II.

DR Pfam; PF00152; tRNA-synt\_2; 1.  
DR Pfam; PF01336; tRNA anti; 1.  
DR PRINTS; PR01042; TRNASYNTHASP.  
DR PRINTS; PR00982; TRNASYNTHLYS.  
DR TIGRFAMs; TIGR00499; lys\_bact; 1.  
DR PROSITE; PS50862; AA tRNA\_LIGASE\_II; 1.  
KW ATP-binding; Aminoacyl-tRNA synthetase; ligase; protein biosynthesis.  
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Best local Similarity 70.6%; Pred. No. 11;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
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Db 19 AEOKAKEKAKAAAPA 35  
  
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AC Q9W327;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE CG12141-PB.  
GN ORFNames=CG12141;  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; *Drosophila*.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Pfeiffer B.D.,  
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
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RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
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RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Williams S.M., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zheng L.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).

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RN [2]
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RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu B., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
DR EMBL; AE003447; AAF46510.2; -.
DR HSSP; P13030; 1BBW.
DR FlyBase; FBgn0027084; Aats-lys.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004815; F:aspartate-tRNA ligase activity; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004824; F:lysine-tRNA ligase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006422; F:aspartyl-tRNA aminoacylation; IEA.
DR GO; GO:0006430; F:lysyl-tRNA aminoacylation; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR004364; tRNA-synt_2.
DR InterPro; IPR002312; tRNA-synt_asp.
DR InterPro; IPR002313; tRNA-synt_lys_2.
DR InterPro; IPR004365; tRNA-anti.
DR InterPro; IPR006195; tRNA_ligase_II.
DR Pfam; PF00152; tRNA-synt_2; 1.
DR Pfam; PF01336; tRNA-anti; 1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR PRINTS; PR00982; TRNASYNTHLYS.
DR TIGRFAMs; TIGR00499; lys_bact; 1.
DR PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
KW ATP-binding; Aminoacyl-tRNA synthetase; ligase; Protein biosynthesis.
SQ SEQUENCE 607 AA; 68503 MW; 771CE9870963D81B CRC64;

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OY 1 APEKAKEAFKAAAPA 17
Db 52 AEQKAKEKAEKAAAPA 68

RESULT 3
ID O9AAC8 PRELIMINARY; PRT; 389 AA.
AC O9AAC8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein CC0674.
GN OrderedLocustNames=CC0674;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Niernan W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005743; AAK22659.1; -.
DR PIR; G87332; G87332.
DR TIGR; CC0674; -.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000897; SRP54.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
DR PROSITE; PS00300; SRP54; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 389 AA; 40769 MW; C6DD05B8CE8D150E CRC64;

Query Match 57.8%; Score 48; DB 2; Length 389;
Best Local Similarity 64.7%; Pred. No. 16;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKEAFKAAAPA 17
Db 63 ADGKTSVETPKAAAPA 79

RESULT 4
ID O916C2 PRELIMINARY; PRT; 465 AA.
AC O916C2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Probable zinc protease.
GN OrderedLocustNames=PA0372;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Watrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,

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RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004475; AAC03761.1; -.
DR PIR; D83598; D83598.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001431; Insulinase like.
DR InterPro; IPR007863; Peptidase_M16_C.
DR Pfam; PF00675; Peptidase_M16; I.
DR Pfam; PF05193; Peptidase_M16_C; 1.
KW Complete proteome; Protease.
SQ SEQUENCE 465 AA; 51975 MW; 8D20E91407605A91 CRC64;

Query Match 55.4%; Score 46; DB 2; Length 465;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 PEKAKFEAFKAAAPA 17
Db 172 PNALAFERFKAAAYPA 187

RESULT 5
Q7M495 PRELIMINARY; PRT; 189 AA.
ID Q7M495
AC Q7M495;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Exoskeletal protein HACP202B (Fragment).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxId=6706;
RN [1]
RP SEQUENCE.
RA Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.;
RL Submitted (JUN-1997) to the PIR data bank.
DR PIR; S77935; S77935.
FT NON_TER 1 1
FT NON_TER 189 189
SQ SEQUENCE 189 AA; 20180 MW; 72A4EFCDD9C7BCFE9 CRC64;

Query Match 54.8%; Score 45.5; DB 2; Length 189;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 12; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 APEKAK-PEAFKAAAPA 17
Db 9 AAEXARFFQAFKAAEAAA 26

RESULT 6
Q7M496 PRELIMINARY; PRT; 189 AA.
ID Q7M496
AC Q7M496;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Exoskeletal protein HACP202A (Fragment).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxId=6706;
RN [1]
RP SEQUENCE.
RA Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.;

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RL Submitted (JUN-1997) to the PIR data bank.
DR PIR; S77930; S77930.
FT NON_TER 1
FT NON_TER 189
SQ SEQUENCE 189 AA; 20154 MW; 72AAEFCD9C647FE9 CRC64;

Query Match 54.8%; Score 45.5; DB 2; Length 189;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 12; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 APEKAK-PEAFKAAAPA 17
   | | | | | | | | | |
Db 9 AAEKARFFQAFKAAEAAA 26

RESULT 7
RL19_AGR15 STANDARD; PRT; 179 AA.
AC Q8UBZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L19.
DN Name=rplS; OrderedLocustNames=Atu2703, AGR_C 4900;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Str.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neeter E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quirello B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Hounzel K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
RN [3]
RP FUNCTION: This protein is located at the 30S-50S ribosomal subunit
RT interface and may play a role in the structure and function of the
RT aminoacyl-tRNA binding site (By similarity).
RN [4]
RP SIMILARITY: Belongs to the ribosomal protein L19 family.
RN [5]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
RN between the Swiss Institute of Bioinformatics and the EMBL outstation -
RN the European Bioinformatics Institute. There are no restrictions on its
RN use by non-profit institutions as long as its content is in no way
RN modified and this statement is not removed. Usage by and for commercial
RN entities requires a license agreement (See http://www.isb-sib.ch/announce/
RN or send an email to license@isb-sib.ch).
RN [6]
RP EMBL; AE009216; AAL43684.1; -
RN EMBL; AE008183; AAK88423.1; -
RN PIR; AF2908; AF2908.
RN PIR; F97683; F97683.

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DR HAMAP; MF\_00402; -. 1.  
 DR InterPro; IPR001857; Ribosomal\_L19.  
 DR Pfam; PF01245; Ribosomal\_L19; 1.  
 DR PRINTS; PR00061; RIBOSOMAL\_L19.  
 DR PRODOM; PD002979; Ribosomal\_L19; 1.  
 DR TIGRFAMs; TIGR01024; rplS\_bact; 1.  
 DR PROSITE; PS01015; RIBOSOMAL\_L19; 1.  
 DR Complete proteome; Ribosomal protein.  
 KW SEQUENCE 179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;

Query Match 54.2%; Score 45; DB 1; Length 179;  
 Best Local Similarity 64.7%; Pred. No. 23;  
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAFEFKRAAAPA 17  
 |||: ||| |||  
 DB 135 ABEKARLEAEKVAAAQA 151

## RESULT 8

ID Q81W24 PRELIMINARY; PRT; 183 AA.  
 AC Q81W24; Q61526; Q6KYS0;  
 DT 01-JUN-2003 (TReMBLrel. 24, Created)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 GN Ordered locus names=BA0013, BAS0016, GBA0013;  
 OS Bacillus anthracis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1392;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Ames / isolate Porton;  
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;  
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,  
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,  
 RA Holtzapfe E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,  
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,  
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niernan W.C.,  
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,  
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,  
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;  
 RT "The genome sequence of Bacillus anthracis Ames and comparison to  
 RT closely related bacteria."  
 RL Nature 423:81-86(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Ames / isolate 0581;  
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,  
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,  
 RA Fraser C.M.;  
 RT "Bacillus anthracis comparative genomics."  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Steine;  
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Oknaka R.,  
 RA Richardson P., Rubin E., Tice H.,  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE017024; AAP24070.1; -.  
 DR EMBL; AE017334; AAT29093.1; -.  
 DR EMBL; AE017225; AAT52355.1; -.

DR TIGR; BA0013; -.

DR InterPro; IPR009058; wing\_hlx\_DNA\_bnd.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 183 AA; 20653 MW; 3BD4AC2C8D658752 CRC64;

Query Match 54.2%; Score 45; DB 2; Length 183;  
 Best Local Similarity 62.5%; Pred. No. 24;  
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAFEFKRAAAP 16  
 |||: ||| |||  
 DB 116 APEKAFEFKRAAAP 131

## RESULT 9

ID Q8PGF8 PRELIMINARY; PRT; 607 AA.  
 AC Q8PGF8;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE dihydroliipoamide dehydrogenase.  
 GN Name=lpda; Ordered locus names=XAC3659;  
 OS Xanthomonas axonopodis (pv. citri).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OX NCBI\_TaxID=92829;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=306 / ATCC 13902 / XV 101;  
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;  
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
 RA Camarotte G., Camavan F., Cardozo J., Chambergo F., Ciapina L.P.,  
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorzy H.,  
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Trufi D., Tsai S.M., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities."  
 RL Nature 417:459-463(2002).

CC -I- CATALYTIC ACTIVITY: Protein N(6)-(dihydrolipoyl)lysine + NAD(+) =  
 CC protein N(6)-(lipoyl)lysine + NADH.

CC -I- COFACTOR: Binds 1 FAD per subunit (By similarity).

CC -I- MISCELLANEOUS: The active site is a redox-active disulfide bond  
 CC (By similarity).

CC -I- SIMILARITY: Belongs to the class-I pyridine nucleotide-disulfide  
 CC oxidoreductase family.

CC -I- SIMILARITY: Contains 1 lipoyl-binding domain.

DR EMBL; AE012016; AAM38502.1; -.

DR HSSP; Q51225; 1OUT.

DR GO; GO:0005737; C:cytoplasm; IEA.

DR GO; GO:0004148; F:dihydrolipoyl dehydrogenase activity; IEA.

DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR GO; GO:0006096; P:glycolysis; IEA.

DR InterPro; IPR000089; Biotin\_lipoyl.

DR InterPro; IPR001327; FAD\_pyr\_redox.

DR InterPro; IPR000815; Hg\_reductase.

DR InterPro; IPR011053; Hybrid\_motif.

DR InterPro; IPR006258; Lipoamide\_dh.

DR InterPro; IPR003016; Lipoyl\_BS.

DR InterPro; IPR000205; NAD\_BS.

DR InterPro; IPR001100; Pyr\_redox.

DR InterPro; IPR004099; Pyr\_redox\_dim.

DR Pfam; PF00364; Biotin\_lipoyl; 1.

DR Pfam; PF00070; Pyr\_redox; 1.

DR Pfam; PF02852; Pyr\_redox\_dim; 1.

DR PRINTS; PR00368; FADPNR.  
 DR PRINTS; PR00945; HGRDTASE.  
 DR PRINTS; PR00411; PNDRDTASEI.  
 DR PRODOM; PD000139; FAD\_pyr\_redox; 1.  
 DR TIGRFAMS; TIGR01350; lipamide\_DH; 1.  
 DR PROSITE; PS00189; LIPOYL; 1.  
 DR PROSITE; PS00076; PYRIDINE\_REDOX\_1; 1.  
 DR Complete proteome; FAD; Flavoprotein; lipoyl; NAD; Oxidoreductase;  
 KW Redox-active center.  
 SQ SEQUENCE 607 AA; 63213 MW; 2D218BCF97903D9F CRC64;

Query Match 54.2%; Score 45; DB 2; Length 607;  
 Best Local Similarity 64.7%; Pred. No. 75;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
 |||:|||||  
 Db 84 APAKAEPRKAPAAAPA 100

## RESULT 10

Q8PSL8 PRELIMINARY; PRT; 836 AA.

AC Q8PSL8; 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
 DE Hypothetical protein MM3061.  
 GN OrderedLocustNames=MM3061;  
 OS Methanosarcina mazel (Methanosarcina frisia).  
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;  
 OC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;  
 RX MEDLINE=2120827; PubMed=12125824;  
 RA Deppeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,  
 RA Martinez-Arias R., Henne A., Wieser A., Baeumer S., Jacobi C.,  
 RA Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,  
 RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,  
 RA Fritz H.-J., Gottschalk G.;  
 RT "The genome of Methanosarcina mazel: evidence for lateral gene  
 transfer between Bacteria and Archaea."  
 RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).  
 DR EMBL; AE013561; AAM32757.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 836 AA; 93347 MW; DFCE3FF75DD0153B CRC64;

Query Match 54.2%; Score 45; DB 2; Length 836;  
 Best Local Similarity 60.0%; Pred. No. 1e+02;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 15  
 |||||:|||||  
 Db 819 APEKGIKIFEAIAAS 833

## RESULT 11

Q7M3W1 PRELIMINARY; PRT; 97 AA.

AC Q7M3W1; 01-MAR-2004 (Tremblrel. 26, Created)  
 DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Repetitive protein antigen 69/70 (Fragment).  
 OS Trypanosoma cruzi.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5693;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89277508; PubMed=2659529;  
 RA Hoff D.F., Kim K.S., Otsu K., Moser D.R., Yost W.J., Blumin J.H.,

RA Donelson J.F., Kirchhoff L.V.;  
 RT "Trypanosoma cruzi expresses diverse repetitive protein antigens."  
 RL Infect. Immun. 57:1959-1967(1989).  
 DR PIR; G60110; G60110.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
 DR GO; GO:0006412; P:protein biosynthesis; IEA.  
 DR InterPro; IPR001859; Ribosomal\_P2.  
 DR PRINTS; PR00456; RIBOSOMALP2.  
 FT NON TER 1 1  
 FT NON TER 97 97  
 SQ SEQUENCE 97 AA; 8210 MW; 477B46BEE0DFE3E2 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 97;  
 Best Local Similarity 64.7%; Pred. No. 19;  
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
 |||:|||||  
 Db 2 APAKAAAPAKAAAPA 18

## RESULT 12

Q87HZ8 PRELIMINARY; PRT; 353 AA.

AC Q87HZ8; 01-JUN-2003 (Tremblrel. 24, Created)  
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Putative periplasmic linker protein.  
 GN OrderedLocustNames=VPA0808;  
 OS Vibrio parahaemolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=670;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;  
 RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;  
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
 RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism  
 distinct from that of V. cholerae."  
 RL Lancet 361:743-749(2003).  
 DR EMBL; AP005086; BAC62151.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0015428; F:type I protein secretor activity; IEA.  
 DR GO; GO:0009306; P:protein secretion; IEA.  
 DR InterPro; IPR006143; HlyD.  
 DR InterPro; IPR003997; RtxD.  
 DR InterPro; IPR011054; Rudmt\_hyb\_motif.  
 DR PRINTS; PR01490; RTXTOXIND.  
 DR TIGRFAMS; TIGR01730; RND\_mfp; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 353 AA; 38932 MW; BBB222D4212CE833 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 353;  
 Best Local Similarity 47.1%; Pred. No. 66;  
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAFKAAAPA 17  
 |||:|||||  
 Db 40 APVKSQYRAFKGLVPA 56

## RESULT 13

O85598 PRELIMINARY; PRT; 390 AA.

AC O85598; 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)



DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Dihydrolipoamide succinyl transferase.  
OS Brucella abortus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=235;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=519;  
RA Boschirol L., Cravero S., Rosetti O.L.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
DR EMBL; AF070932; AAC23605.1; -.  
DR HSSP; P07016; 1C4T.  
DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. . .; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.  
DR InterPro; IPR001078; 2Oxoacid dh.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR004167; E3 binding.  
DR InterPro; IPR011053; Hybrid\_motif.  
DR InterPro; IPR006255; SucB.  
DR Pfam; PF00198; 2-oxoacid\_dh; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF02817; E3\_binding; 1.  
DR ProDom; PD001115; 2Oxoacid\_dh; 1.  
DR TIGRFAMs; TIGR01347; sucB; 1.  
KW Acyltransferase; Lipoyl; Transferase.  
SQ SEQUENCE 390 AA; 41004 MW; 5A0AAD87569F5C2 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 390;  
Best Local Similarity 64.7%; Pred. No. 72;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APEKAKFEAFKAAAPA 17  
Db 71 APAQKKEAKPAAAPA 87

RESULT 14  
Q8FYF8 PRELIMINARY; PRT; 408 AA.  
ID Q8FYF8  
AC Q8FYF8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE 2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide  
DE succinyltransferase (EC 2.3.1.61).  
GN Name=sucB; OrderedLocustNames=BR1922;  
OS Brucella suis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29461;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1330 / Biovar 1;  
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;  
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,  
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,  
RA Van Aken S.E., Riedmiller S., Tettelin H., Gill S.R., White O.,  
RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,  
RA Fraser C.M.;  
RT "The Brucella suis genome reveals fundamental similarities between  
RT animal and plant pathogens and symbionts.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).  
CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.

DR EMBL; AE014482; AAN30814.1; -.  
DR HSSP; P07016; 1C4T.  
DR TIGR; BR1922; -.  
DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. . .; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.  
DR InterPro; IPR001078; 2Oxoacid dh.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR004167; E3 binding.  
DR InterPro; IPR011053; Hybrid\_motif.  
DR InterPro; IPR003016; Lipoyl\_BS.  
DR InterPro; IPR006255; SucB.  
DR Pfam; PF00198; 2-oxoacid\_dh; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF02817; E3\_binding; 1.  
DR ProDom; PD001115; 2Oxoacid\_dh; 1.  
DR TIGRFAMs; TIGR01347; sucB; 1.  
DR PROSITE; PS00189; LIPOYL; 1.  
KW Acyltransferase; Complete proteome; Lipoyl; Transferase.  
SQ SEQUENCE 408 AA; 42839 MW; 7EC80A61800ACC64 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 408;  
Best Local Similarity 64.7%; Pred. No. 75;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APEKAKFEAFKAAAPA 17  
Db 86 APAQKKEAKPAAAPA 102

RESULT 15  
Q9L6H8 PRELIMINARY; PRT; 408 AA.  
ID Q9L6H8  
AC Q9L6H8; Q7CNV5;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE  
DE DEHYDROGENASE COMPLEX (EC 2.3.1.61).  
GN Name=sucB; OrderedLocustNames=BMEI0141;  
OS Brucella melitensis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29459;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=16M;  
RX MEDLINE=21437665; PubMed=11553602;  
RX DOI=10.1128/IAI.69.10.6537-6540.2001;  
RX Zymunt M.S., Diaz M.A., Teixeira-Gomes A.P., Cloeckaert A.;  
RT "Cloning, nucleotide sequence, and expression of the Brucella  
RT melitensis sucB gene coding for an immunogenic dihydrolipoamide  
RT succinyltransferase homologous protein.";  
RL Infect. Immun. 69:6537-6540(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=16M / ATCC 23456 / Biotype 1;  
RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;  
RX Delvecchio V.G., Kapratel V., Redkar R.J., Patra G., Mujer C., Los T.,  
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,  
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,  
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
RA Haselkorn R., Kyrpides N.C., Overbeek R.;  
RT "The genome sequence of the facultative intracellular pathogen  
RT Brucella melitensis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.  
DR EMBL; AF235020; AAF43701.1; -.  
DR EMBL; AE009457; AAL51323.1; -.

DR PIR; AH3269; AH3269.  
DR HSSP; P07016; 1C4T.  
DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0004149; F:diacylglycerol 3-phosphate succinyltransferase; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.  
DR InterPro; IPR01078; 2-oxoacid dh.  
DR InterPro; IPR000089; Biotin lipoyl.  
DR InterPro; IPR004167; E3 binding.  
DR InterPro; IPR011053; Hybrid motif.  
DR InterPro; IPR003016; Lipoyl\_BS.  
DR InterPro; IPR006255; SUCB.  
DR Pfam; PF00198; 2-oxoacid dh; 1.  
DR Pfam; PF00364; Biotin lipoyl; 1.  
DR Pfam; PF02817; E3 binding; 1.  
DR ProDom; PD001115; 2-oxoacid dh; 1.  
DR TIGRfam; TIGR01347; sucB; 1.  
DR PROSITE; PS00189; LIPOYL; 1.  
DR Acyltransferase; Complete proteome; Lipoyl; Transferase.  
KW ACYLTRANSFERASE; Complete proteome; Lipoyl; Transferase.  
SQ SEQUENCE 408 AA; 42911 MW; 16E763942B097CA7 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 408;  
Best Local Similarity 64.7%; Pred. No. 75;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Oy 1 APEKAKFEAKFAAAPA 17  
Db 86 APAQKKEAKFAAAPA 102

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Job time : 128.906 secs